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OM nucleic - nucleic search, using sw model

Run on: July 4, 2003, 00:36:13 ; Search time 456 Seconds
(without alignments)
9951.264 Million cell updates/sec

Title: US-10-007-010-3
Perfect score: 2015
Sequence: 1 cggaggcagcgaagatgagg.....ataataatgcaatcttaag 2015

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2015	100.0	2015	24	ABK83939 Human cDNA differe
2	2015	100.0	2015	24	ABL66673 Lung cancer relate
3	1552	77.0	1926	24	ABK83940 Human cDNA differe
4	183	9.1	183	24	ABL61214 Human nucleotide f
5	181	9.0	1416	24	ABL61215 Rat/human fusion c
6	181	9.0	1542	24	ABL61216 Rat/human fusion c
7	169	8.4	369	16	NA119957 Human gene signatu
8	133	6.6	171	22	ABA50558 Human breast cell
9	133	6.6	171	22	ABA68516 Human foetal liver

10	133	6.6	171	22	ABA35497 Probe #13963 for g
11	133	6.6	171	22	AAK16884 Human brain expres
12	133	6.6	171	22	AAK42654 Human bone marrow
13	133	6.6	171	22	AAI23408 Probe #13341 for g
14	133	6.6	171	22	AAI48728 Probe #17414 used t
15	133	6.6	171	22	AAI09035 Probe #9026 used t
16	133	6.6	171	22	ABS16706 Human genome-deriv
17	113	5.6	415	22	ABA45430 Human breast cell
18	113	5.6	415	22	ABA55928 Human foetal liver
19	113	5.6	415	22	ABA25595 Human foetal liver
20	113	5.6	415	22	AAK04142 Human brain expres
21	113	5.6	415	22	AAK29623 Human bone marrow
22	113	5.6	415	22	AAI14202 Probe #4135 for ge
23	113	5.6	415	22	AAI35583 Probe #4269 used t
24	113	5.6	415	22	AAI04039 Probe #4030 used t
25	113	5.6	415	24	ABS04179 Human genome-deriv
26	112	5.6	1592	20	AAZ227241 Human secreted pro
27	78	3.9	409	22	AAH99174 Human protein enco
28	77	3.8	334	21	AAAS2650 Eosinophil activat
29	68	3.4	1911	24	ABK63704 Rat sequence diff
30	66	3.3	274	22	AAK68573 Human immune/haema
31	65	3.2	1926	24	ABK83940 Human cDNA differe
32	31	1.5	31	22	AAI30734 Human single nucle
33	31	1.5	31	22	AAI30735 Human single nucle
34	31	1.5	31	22	AAI30736 Human single nucle
35	31	1.5	31	22	AAI30737 Human single nucle
36	31	1.5	31	22	AAI30738 Human single nucle
37	28	1.4	2298	24	ABK83935 Human cDNA differe
38	27	1.3	33	22	AAH41498 Human tyrosine kin
39	26	1.3	32	22	AAH41491 Human tyrosine kin
40	26	1.3	32	22	AAH41492 Human tyrosine kin
41	26	1.3	1602	14	AAQ46687 Chicken pp60 c-src
42	26	1.3	1759	21	AAZ29700 Wild-type chicken
43	26	1.3	1759	22	AAH28357 Nucleotide sequenc
44	25	1.2	32	22	AAH41501 Human tyrosine kin
45	25	1.2	51	23	ABL00375 Human silent nonco

ALIGNMENTS

RESULT 1
ABK83939
ID ABK83939 standard; cDNA; 2015 BP.
AC AC
XX ABK83939;
XX DT 14-AUG-2002 (first entry)
XX DE Human cDNA differentially expressed in granulocytic cells #510.
DE DE
XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW KW viral infection; parasitic infection; protozoal infection;
KW KW fungal infection; sterile inflammatory disease; psoriasis;
KW KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW KW adult respiratory distress syndrome; inflammatory bowel disease;
KW KW Crohn's disease; ulcerative colitis; periodontal disease;
KW KW granulocyte activation; chronic inflammation; allergy.
XX OS Homo sapiens.
XX PN WO200228999-A2.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US30821.
XX PR 03-OCT-2000; 2000US-237189P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

Db 1381 CCTGAAGCCATCAACTTTGGCTCTTCCACCATCAAGTCAGACGCTCTGGTCTCTTGGTATC 1440
QY 1441 CTGCTGATGGAGATCGTCACCTAGGCGCGGATCCCTTACCCAGGATGTCAAACCTCGAA 1500
Db 1441 CTGCTGATGGAGATCGTCACCTAGGCGCGGATCCCTTACCCAGGATGTCAAACCTCGAA 1500
QY 1501 GTGATCCGAGCTCTGGAGCGTGGATACCGGATCGCTCGCCAGAGAACTGCCAGAGGAG 1560
Db 1501 GTGATCCGAGCTCTGGAGCGTGGATACCGGATCGCTCGCCAGAGAACTGCCAGAGGAG 1560
QY 1561 CTCCTACACATCATGATCGCTGTGGAAAAACCGTCCGGAGGAGCGCCGACTTCGAA 1620
Db 1561 CTCCTACACATCATGATCGCTGTGGAAAAACCGTCCGGAGGAGCGCCGACTTCGAA 1620
QY 1621 TACATCCAGAGTGTCTGGATGACTTCTACACGGCCACAGAGAGCCAGTACCAACAGCAG 1680
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QY 1681 CCATGATAGGAGGAGCAGGCGAGGCGGAGGCGTCCAGGTGGTGGCTCGAAAGGTGGCT 1740
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QY 1801 AGCCACAGTTCCTCATCTGCTCCAGTGGTGGTGGAGTGGAGTGGAAATCTCTTTTGACTC 1860
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QY 1861 TTGCAATCCACAATCTGACATTCAGGAAGCCGCCAAGTTGATATTTCTTCCTGGA 1920
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QY 1921 ATGGTTGGATTTAGTTACAGCTGTGATTTGGAAGGAACTTCAAAATAGTGAATGA 1980
Db 1921 ATGGTTGGATTTAGTTACAGCTGTGATTTGGAAGGAACTTCAAAATAGTGAATGA 1980
QY 1981 ATATTAAATAAAGATATAATCAAGTCTTAGC 2015
Db 1981 ATATTAAATAAAGATATAATCAAGTCTTAGC 2015

RESULT 2
ABL66673
ID ABL66673 standard; DNA; 2015 BP.
XX
AC ABL66673;
XX
XX
DT 15-MAY-2002 (first entry)
DE Lung cancer related gene sequence SEQ ID NO:5010.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
XX WO200194629-A2.
PN
XX
PD 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.

20-SEP-2000; 2000US-234052P.
22-SEP-2000; 2000US-234509P.
22-SEP-2000; 2000US-234567P.
25-SEP-2000; 2000US-234923P.
25-SEP-2000; 2000US-234924P.
25-SEP-2000; 2000US-235077P.
25-SEP-2000; 2000US-235082P.
25-SEP-2000; 2000US-235134P.
25-SEP-2000; 2000US-235280P.
25-SEP-2000; 2000US-235637P.
26-SEP-2000; 2000US-235638P.
27-SEP-2000; 2000US-235711P.
27-SEP-2000; 2000US-235720P.
27-SEP-2000; 2000US-235840P.
27-SEP-2000; 2000US-235863P.
28-SEP-2000; 2000US-236028P.
28-SEP-2000; 2000US-236032P.
28-SEP-2000; 2000US-236033P.
28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236109P.
29-SEP-2000; 2000US-236111P.
29-SEP-2000; 2000US-236842P.
29-SEP-2000; 2000US-236891P.
02-OCT-2000; 2000US-237172P.
02-OCT-2000; 2000US-237173P.
02-OCT-2000; 2000US-237278P.
02-OCT-2000; 2000US-237294P.
02-OCT-2000; 2000US-237295P.
02-OCT-2000; 2000US-237316P.
03-OCT-2000; 2000US-237425P.
03-OCT-2000; 2000US-237598P.
03-OCT-2000; 2000US-237604P.
03-OCT-2000; 2000US-237606P.
03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
DR
XX
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 5010; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 2015 BP; 512 A; 540 C; 580 G; 383 T; 0 other;
Query Match 100.0%; Score 2015; DB 24; Length 2015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAGGCCAGCAAGATGAGGAAGATGATCAGGAGGATGATCAAGGTGAAGGAGATGA 60
Db 1 CGAGGCCAGCAAGATGAGGAAGATGATCAGGAGGATGATCAAGGTGAAGGAGATGA 60
QY 61 AGAGCATGACGACGATGCTCTGAGGGAGCCTCAGGGGCTGCCAGAGTGGGGGGGGCTC 120
Db 61 AGAGCATGACGACGATGCTCTGAGGGAGCCTCAGGGGCTGCCAGAGTGGGGGGGGCTC 120
QY 121 AAGCTGGGAGATCCGGGCTGCCCGGAGACGAGGAGCGGGCCAGGATGGGGTGCATG 180
Db 121 AAGCTGGGAGATCCGGGCTGCCCGGAGACGAGGAGCGGGCCAGGATGGGGTGCATG 180
QY 181 AAGTCCAAAGTTCTCCAGGTCGGAGCAATACATTTCTCAAAATCTGAACCCAGCGCCAGC 240
Db 181 AAGTCCAAAGTTCTCCAGGTCGGAGCAATACATTTCTCAAAATCTGAACCCAGCGCCAGC 240
QY 241 CCACACTGCTGTGTAGCTGCGGATCCACATCCACATCCACATCAAGCGGGGCTAATAGC 300
Db 241 CCACACTGCTGTGTAGCTGCGGATCCACATCCACATCCACATCAAGCGGGGCTAATAGC 300
QY 301 CACAAAGCAACACACAGCAATCAGGAGCGAGGCTCTGAGACATCATCTGCTGGTGC 360
Db 301 CACAAAGCAACACACAGCAATCAGGAGCGAGGCTCTGAGACATCATCTGCTGGTGC 360
QY 361 CTGTATGATTACGAGGCCATTCACCAAGAACCTCAGCTTCCAGAGGGGGACACAGATG 420
Db 361 CTGTATGATTACGAGGCCATTCACCAAGAACCTCAGCTTCCAGAGGGGGACACAGATG 420
QY 421 GTGGTCTCTAGAGGAATCCGGGAGTGTGGAAGGCTCGATCCCTGGCCACCGGAGGAG 480
Db 421 GTGGTCTCTAGAGGAATCCGGGAGTGTGGAAGGCTCGATCCCTGGCCACCGGAGGAG 480
QY 481 GGCTACATCCAAAGCAACTATGTCGCCGGTGTGACTCTCTGGAGACAGAGGATGGTTT 540
Db 481 GGCTACATCCAAAGCAACTATGTCGCCGGTGTGACTCTCTGGAGACAGAGGATGGTTT 540
QY 541 TTCAAGGGCATCAGCGGAAGGACGAGCGGCAACTCTGCTCCCGGCAACATGCTG 600
Db 541 TTCAAGGGCATCAGCGGAAGGACGAGCGGCAACTCTGCTCCCGGCAACATGCTG 600
QY 601 GGCTCTCTATGATCCGGGATAGCGAGACCACTAAAGGAAGCTACTTTTGTCCGTGCGA 660
Db 601 GGCTCTCTATGATCCGGGATAGCGAGACCACTAAAGGAAGCTACTTTTGTCCGTGCGA 660
QY 661 GACTACAGCCTCGGAGGAGATACCGTGAACATTTACAAGATCCGGACCTGGACAAC 720
Db 661 GACTACAGCCTCGGAGGAGATACCGTGAACATTTACAAGATCCGGACCTGGACAAC 720
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Db 721 GGGGGCTTTCTACATATCCCGGAGGAGTCTGCGTGCCTGCAATGCTTCCCAAG 780
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Db 781 TACAAGAGGGGAGCAAGGCTCTGCCAGAACTCTGCTGCTGCAATGCTTCCCAAG 840
QY 841 CCCAGAGCCTTGGGAGAAAGTCCCTGGAGATCCCTCGGGAATCCCTCAAGCTGGAG 900
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Db 1201 GCAGAGGATCGGCTTTCATCAGCAGAGGAATACATCCACCGAGAGCTCCGAGCTGCC 1260
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Db 1261 AACATCTTGGTCTCTGCATCCCTGCTGTGTAGATTGCTGACTTTGGCTTGGCCCGGGTC 1320
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Db 1321 ATTGAGGACAAGAGTACACGCTCGGGAAGGGGCAAGTTCCCATCAAGTGGACAGCT 1380
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Db 1381 CCTGAAGCCATCAACTTTGGCTTCCATCAAGTCAAGTCAAGTCTGCTTGGTATC 1440
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Db 1441 CTGCTGATGGAGATCGTCACTACGCGGATCCCTTACCCAGGAGTGTCAAAACCTGAA 1500
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Db 1501 GTGATCCAGCTCTGGAGCGTGGATACCGGATGCTCCGAGAGAACTGCCAGAGAG 1560
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Db 1561 CTCTACAACATCATGATCGCTGTGGAAAACCGTCCGGAGGAGCGGCGACCTCGAA 1620
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Db 1621 TACATCCAGAGTGTGCTGGATGACTTCTACAGGCCACAGAGAGCCAGTACCAACAGCAG 1680
QY 1681 CCATGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
Db 1681 CCATGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
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Db 1741 CCAGCAGCATCCGCGAGGCGCCACACCCCTTCCCTACTCCAGACACCCACCTCGCTTC 1800
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Db 1801 AGCCACAGTTTCTCTCATCTGTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1860
QY 1861 TTGCAATCCCAATCTGACATTTCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Db 1861 TTGCAATCCCAATCTGACATTTCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
QY 1921 ATGTTGGATTTTGTAGTTACAGCTGTGATTTGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Db 1921 ATGTTGGATTTTGTAGTTACAGCTGTGATTTGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 ATATTTAAATAAAGATATAAATGCAAGTCTTACG 2015
Db 1981 ATATTTAAATAAAGATATAAATGCAAGTCTTACG 2015

RESULT 3

ABK83940

ID ABK83940 standard; cDNA; 1926 BP.

AC ABK83940;

XX

DT 14-AUG-2002 (first entry)

XX

Human cDNA differentially expressed in granulocytic cells #511.

Human; ss; granulocytic cell; DNA chip; bacterial infection;
viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
cardiac reperfusion injury; renal reperfusion injury; ARDS;
adult respiratory distress syndrome; inflammatory bowel disease;
Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US30821.

03-OCT-2000; 2000US-237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression
of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states and
drug toxicity

Claim 1; SEQ ID No 511; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
DNA chip analysis as given in the specification, and comparing
the expression level to an expression level in an unactivated
GC, where differential expression of Gs is indicative of GCA.

Also included are modulation of at least one gene in Gs; (2) screening (M3)
for an agent capable of modulating GCA or an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease using the
gene expression profile; (3) detecting (M4) an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease, by detecting the
level of expression in a sample of the tissue of gene(s) from Gs, where
the level of expression of the gene is indicative of inflammation;

(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
modulating GCA; M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for

detecting an inflammation (especially chronic) in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
reperfusion injury, ARDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
periodontal disease; also bacterial infection, viral infection,
parasitic infection, protozoal infection, fungal infection and M5 is
useful for treating one of the above conditions. The present
sequence represents a gene differentially expressed in granulocytes.

Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 1926 BP; 497 A; 522 C; 520 G; 387 T; 0 other;

Query Match		77.0%;	Score 1552;	DB 24;	Length 1926;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1552;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	178	ATGAAGTCCAAGTTCTCCAGTCCGAGGCAATACATTTCTCAAAAACTGAAACACGCGC	237		
Db	85	ATGAAGTCCAAGTTCTCCAGTCCGAGGCAATACATTTCTCAAAAACTGAAACACGCGC	144		
QY	238	AGCCACACATGTCTGTGTACGTCCGGATCCACATCCACCATCAAGCGGGGCTAAT	297		
Db	145	AGCCACACATGTCTGTGTACGTCCGGATCCACATCCACCATCAAGCGGGGCTAAT	204		
QY	298	AGCCACACACAGCAACACACAGGAATCAGGAGGAGGCTCTCAGGACATCATCTGGTGT	357		
Db	205	AGCCACACACAGCAACACACAGGAATCAGGAGGAGGCTCTCAGGACATCATCTGGTGT	264		
QY	358	GCCTGTATGATTACGAGGCCATTACACGAAAGACCTCAGCTTCCAGAGGGGACACAG	417		
Db	265	GCCTGTATGATTACGAGGCCATTACACGAAAGACCTCAGCTTCCAGAGGGGACACAG	324		
QY	418	ATGGTGTCTTAGAGGAATCCGGGGAGTGGTGAAGGCTCGATCCCTGGCCACCCGGAAG	477		
Db	325	ATGGTGTCTTAGAGGAATCCGGGGAGTGGTGAAGGCTCGATCCCTGGCCACCCGGAAG	384		
QY	478	GAGGGTCTACATCCCAAGCAACTATGTCCGCCGCTTGAATCTCTGAGACAGAGGAGTG	537		
Db	385	GAGGGTCTACATCCCAAGCAACTATGTCCGCCGCTTGAATCTCTGAGACAGAGGAGTG	444		
QY	538	TTTTTCAAGGGCATCAGCCGGAAGGACGACGAGCCCAACTGCTGCTCCCGGCAACATG	597		
Db	445	TTTTTCAAGGGCATCAGCCGGAAGGACGACGAGCCCAACTGCTGCTCCCGGCAACATG	504		
QY	598	CTGGGTCTCTCATGATCCGGGATAGGAGACCACTAAAGGAGCTACTTTTGTCCTG	657		
Db	505	CTGGGTCTCTCATGATCCGGGATAGGAGACCACTAAAGGAGCTACTTTTGTCCTG	564		
QY	658	CGAGCTACGACCTCGGACGAGGAGATACCGTGAACATTTACAAGATCCGGACCCCTGGAC	717		
Db	565	CGAGCTACGACCTCGGACGAGGAGATACCGTGAACATTTACAAGATCCGGACCCCTGGAC	624		
QY	718	AAGGGGGCTTCTACATATCCCTCCGAGACCTTCAGACACTCTGAGGAGCTGTGTGAC	777		
Db	625	AAGGGGGCTTCTACATATCCCTCCGAGACCTTCAGACACTCTGAGGAGCTGTGTGAC	684		
QY	778	CACCTACAAGAGGGGACGAGGCTCTGCAGAAACTGTGGTGCCTGCATGTCTTCC	837		
Db	685	CACCTACAAGAGGGGACGAGGCTCTGCAGAAACTGTGGTGCCTGCATGTCTTCC	744		
QY	838	AAGCCCGAGAGCCTTTGGGAGAAAGATGCTGGAGATCCCTCGGGAATCCCTCAAGCTG	897		
Db	745	AAGCCCGAGAGCCTTTGGGAGAAAGATGCTGGAGATCCCTCGGGAATCCCTCAAGCTG	804		
QY	898	GAGAGAAACTTGGAGCTGGGAGTTTGGGAGTCTGGATGCCACCTACACAGAC	957		
Db	805	GAGAGAAACTTGGAGCTGGGAGTTTGGGAGTCTGGATGCCACCTACACAGAC	864		
QY	958	ACCAAGGTGGCAGTGAAGACGATGAAGCCAGGAGGATGCTGGTGGAGGCTTCTTGGCA	1017		
Db	865	ACCAAGGTGGCAGTGAAGACGATGAAGCCAGGAGGATGCTGGTGGAGGCTTCTTGGCA	924		
QY	1018	GAGGCAAGGTGATGAAAACTCTGCAGCATGACAAAGCTGTGCAAACTCATCGGTGTC	1077		
Db	925	GAGGCAAGGTGATGAAAACTCTGCAGCATGACAAAGCTGTGCAAACTCATCGGTGTC	984		
QY	1078	ACCAAGGAGCCCATCTACATCATCAGGAGTTTCATGGCCAAAGAGGCTGTGTGACTTT	1137		
Db	985	ACCAAGGAGCCCATCTACATCATCAGGAGTTTCATGGCCAAAGAGGCTGTGTGACTTT	1044		
QY	1138	CTGAAAGTGTAGGCGCAGCAGCAGCATTTGCCAAAACTCATTTGACTTCTCAGCCAG	1197		
Db	1045	CTGAAAGTGTAGGCGCAGCAGCAGCATTTGCCAAAACTCATTTGACTTCTCAGCCAG	1104		
QY	1198	ATTGCAAGAGGCGATGCCCTTTCATCGAGCAGAGAACTACATCCACCGAGACCTCCGAGCT	1257		

PT diagnosis of acquired immune deficiency syndrome, has high specificity
PT and affinity
XX
PS Claim 13; Page 14-15; 22pp; German.

XX
XX This invention describes a novel fusion protein for blocking the Nef

CC protein of human immune deficiency virus (HIV) which comprises: (i)
CC protein domain 1 that binds to a di-leucine (LL) motif; (ii) a
CC protein domain 2 that binds to a PxxP motif; and (iii) a polypeptide
CC linker between protein domains 1 and 2. The products of the invention
CC have virucide and anti-HIV activity and are capable of neutralising Nef,
CC an accessory protein essential for pathogenicity of HIV-1. The fusion
CC protein of the invention comprises the LL domain of the beta-subunit of
CC the adapter-protein complex Ap-1 and the PxxP binding SH3 domain of
CC tyrosine kinase Hck, linked through a 60 amino acid peptide. The products
CC of the invention are used for in vitro diagnosis of AIDS and for
CC treatment of AIDS. The LL and PxxP motifs are specific for Nef, which,
CC unlike HIV protease, has no human homologue, so the fusion protein (which
CC binds Nef with very high affinity) should cause essentially no side
CC effects. This sequence represents a fusion construct composed of a rat
CC nucleotide fragment which contains a dileucine (LL) motif and a human
CC nucleotide fragment containing a PXXP-motif binding domain useful to the
CC invention.

XX Sequence 1416 BP; 340 A; 383 C; 386 G; 307 T; 0 other;

Query Match 9.0%; Score 181; DB 24; Length 1416;

Best Local Similarity 100.0%; Pred. No. 1.8e-78;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TGAGGACATCATCGTGGTGGCCCTGTATGATTACGAGGCCATTCCACCAGAGCCTCAG 398

DB 1233 TGAGGACATCATCGTGGTGGCCCTGTATGATTACGAGGCCATTCCACCAGAGCCTCAG 1292

QY 399 CTTCCAGAGGGGACCGACAGATGGTCTCTAGAGGAATCCGGGAGTGTTGGAGGCTCG 458

DB 1293 CTTCCAGAGGGGACCGACAGATGGTCTCTAGAGGAATCCGGGAGTGTTGGAGGCTCG 1352

QY 459 ATCCCTGGCCACCCGGAAGGGGCTACATCCCAAGCAACTATGTCGCCCGGTTGACTC 518

DB 1353 ATCCCTGGCCACCCGGAAGGGGCTACATCCCAAGCAACTATGTCGCCCGGTTGACTC 1412

QY 519 T 519

DB 1413 T 1413

RESULT 6

ABL61216
ID ABL61216 standard; DNA; 1542 BP.

XX
XX ABL61216;

DT 04-SEP-2002 (first entry)

XX Rat/human fusion construct capable of inactivating HIV Nef protein.

DE Nef protein; fusion protein; virucide; anti-HIV; accessory protein;

XX pathogenicity; diagnosis; AIDS; rat; human; ds.

XX Rattus sp.

OS Homo sapiens.

OS Synthetic.

XX DE10109532-C1.

XX 13-JUN-2002.

XX 28-FEB-2001; 2001DE-1009532.

XX 28-FEB-2001; 2001DE-1009532.

XX (GEYE/) GEYER M.

PA (FACK/) FACKLER O.

XX Geyer M;

XX WPI; 2002-418264/45.

XX New fusion protein that blocks Nef protein, useful for treatment or
PT diagnosis of acquired immune deficiency syndrome, has high specificity
PT and affinity

XX Claim 16; Page 15-16; 22pp; German.

XX This invention describes a novel fusion protein for blocking the Nef
CC protein of human immune deficiency virus (HIV) which comprises: (i)
CC protein domain 1 that binds to a di-leucine (LL) motif; (ii) a
CC protein domain 2 that binds to a PxxP motif; and (iii) a polypeptide
CC linker between protein domains 1 and 2. The products of the invention
CC have virucide and anti-HIV activity and are capable of neutralising Nef,
CC an accessory protein essential for pathogenicity of HIV-1. The fusion
CC protein of the invention comprises the LL domain of the beta-subunit of
CC the adapter-protein complex Ap-1 and the PxxP binding SH3 domain of
CC tyrosine kinase Hck, linked through a 60 amino acid peptide. The products
CC of the invention are used for in vitro diagnosis of AIDS and for
CC treatment of AIDS. The LL and PxxP motifs are specific for Nef, which,
CC unlike HIV protease, has no human homologue, so the fusion protein (which
CC binds Nef with very high affinity) should cause essentially no side
CC effects. This sequence represents a fusion construct composed of a rat
CC nucleotide fragment which contains a dileucine (LL) motif and a human
CC nucleotide fragment containing a PXXP-motif binding domain useful to the
CC invention.

XX Sequence 1542 BP; 369 A; 419 C; 427 G; 327 T; 0 other;

Query Match 9.0%; Score 181; DB 24; Length 1542;

Best Local Similarity 100.0%; Pred. No. 1.8e-78;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TGAGGACATCATCGTGGTGGCCCTGTATGATTACGAGGCCATTCCACCAGAGCCTCAG 398

DB 1290 TGAGGACATCATCGTGGTGGCCCTGTATGATTACGAGGCCATTCCACCAGAGCCTCAG 1349

QY 399 CTTCCAGAGGGGACCGACAGATGGTCTCTAGAGGAATCCGGGAGTGTTGGAGGCTCG 458

DB 1350 CTTCCAGAGGGGACCGACAGATGGTCTCTAGAGGAATCCGGGAGTGTTGGAGGCTCG 1409

QY 459 ATCCCTGGCCACCCGGAAGGGGCTACATCCCAAGCAACTATGTCGCCCGGTTGACTC 518

DB 1410 ATCCCTGGCCACCCGGAAGGGGCTACATCCCAAGCAACTATGTCGCCCGGTTGACTC 1469

QY 519 T 519

DB 1470 T 1470

RESULT 7

AAT19957

ID AAT19957 standard; cDNA to mRNA; 369 BP.

XX
XX AAT19957;

XX 17-JUL-1996 (first entry)

XX Human gene signature HUMGS01089.

XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;

XX human; cloning; mapping; non-biased library; diagnosis; detection;

XX cell typing; abnormal cell function; ss.

XX Homo sapiens.

XX W09514772-Al.

XX 01-JUN-1995.

XX 11-NOV-1994; 94WO-JP01916.
XX
XX
PR 12-NOV-1993; 93JP-0355504.
XX
XX (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
XX Matsubara K, Okubo K;
PI
XX
XX WPI; 1995-206931/27.
DR
XX
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
XX
PS Claim 1; Page 520; 2245pp; Japanese.
XX
XX A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-#26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
XX Sequence 369 BP; 82 A; 97 C; 102 G; 75 T; 13 other;
SQ
Query Match 8.4%; Score 169; DB 16; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.4e-72;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1535 CTCGCCCCAGAGAACTGCCAGAGGAGCTCTACACATCATGATGCGCTCTGGAAAAACC 1594
DB 33 CTCGCCCCAGAGAACTGCCAGAGGAGCTCTACACATCATGATGCGCTCTGGAAAAACC 92
QY 1595 GTCGGGAGGAGCGCGGACCTTCGAATACATCCAGAGTGTGCTGATGACTTCTACACGG 1654
DB 93 GTCGGGAGGAGCGCGGACCTTCGAATACATCCAGAGTGTGCTGATGACTTCTACACGG 152
QY 1655 CCACAGAGAGCCAGTACCAACAGCAGCCATGATAGGAGGACCGAGGCA 1703
DB 153 CCACAGAGAGCCAGTACCAACAGCAGCCATGATAGGAGGACCGAGGCA 201
RESULT 8
ABA50558
ID ABA50558 standard; DNA; 171 BP.
XX
AC ABA50558;
XX
XX 01-FEB-2002 (first entry)
DT
XX Human breast cell single exon nucleic acid probe #9253.
DE
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200157271-A2.
PN
XX 09-AUG-2001.
PD
XX
XX

PF 30-JAN-2001; 2001WO-US00662.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-496933/54.
DR
XX
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 4; SEQ ID NO 9253; 327pp + sequence listing; English.
PS
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1352 GGGCCAAAGTTCCTCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCA 1411
DB 1 GGGCCAAAGTTCCTCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCA 60
QY 1412 TCAAGTCAGAGCTGTGGTCTTGTGATCTGCTGATGGAGATCGTACCTACGGCGGA 1471
DB 61 TCAAGTCAGAGCTGTGGTCTTGTGATCTGCTGATGGAGATCGTACCTACGGCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133
RESULT 9
ABA68516
ID ABA68516 standard; DNA; 171 BP.
XX
XX ABA68516;
XX
XX 01-FEB-2002 (first entry)
DT
XX Human foetal liver single exon nucleic acid probe #16821.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW
XX Homo sapiens.
OS

```
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF
XX PR 30-JAN-2001; 2001WO-US00666.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488899/53.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts -
XX PS Claim 4; SEQ ID NO 13963; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 1411
Db 1 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 60
; QY 1412 TCAAGTCAGACGCTGGTCTTGGTATCCTGCTGATGGAGATCGTCACCTACGCCCGGA 1471
Db 61 TCAAGTCAGACGCTGGTCTTGGTATCCTGCTGATGGAGATCGTCACCTACGCCCGGA 120
QY 1472 TCCCTTACCCAGG 1484
Db 121 TCCCTTACCCAGG 133

RESULT 10
ABA35497
ID ABA35497 standard; DNA; 171 BP.
XX AC ABA35497;
XX XX
XX DT 23-JAN-2002 (first entry)
XX DE Probe #13963 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX XX

PD XX 09-AUG-2001.
PF XX
PR XX 30-JAN-2001; 2001WO-US00666.
PR XX 04-FEB-2000; 2000US-0180312.
PR XX 26-MAY-2000; 2000US-0207456.
PR XX 30-JUN-2000; 2000US-0608408.
PR XX 03-AUG-2000; 2000US-0632366.
PR XX 21-SEP-2000; 2000US-0234687.
PR XX 27-SEP-2000; 2000US-0236359.
PR XX 04-OCT-2000; 2000GB-0024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488899/53.
DR Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
PS Claim 4; SEQ ID NO 13963; 530pp; English.
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 1411
Db 1 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 60
; QY 1412 TCAAGTCAGACGCTGGTCTTGGTATCCTGCTGATGGAGATCGTCACCTACGCCCGGA 1471
Db 61 TCAAGTCAGACGCTGGTCTTGGTATCCTGCTGATGGAGATCGTCACCTACGCCCGGA 120
QY 1472 TCCCTTACCCAGG 1484
Db 121 TCCCTTACCCAGG 133

RESULT 11
AAK16884
ID AAK16884 standard; DNA; 171 BP.
XX AC AAK16884;
XX XX
XX DT 05-NOV-2001 (first entry)
XX DE Human brain.expressed single exon probe SEQ ID NO: 16875.
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX XX
```

```
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 16875; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
XX
XX Query Match 6.6%; Score 133; DB 22; Length 171;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-55;
XX Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1352 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 1411
DB 1 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 60
QY 1412 TCAAGTCAGACGCTCGTCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 1471
DB 61 TCAAGTCAGACGCTCGTCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133
XX
RESULT 12
AAK42654
ID AAK42654 standard; DNA; 171 BP.
XX
XX AAK42654;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 17211.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 16875; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
XX
XX Query Match 6.6%; Score 133; DB 22; Length 171;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-55;
XX Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1352 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 1411
DB 1 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 60
QY 1412 TCAAGTCAGACGCTCGTCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 1471
DB 61 TCAAGTCAGACGCTCGTCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133
XX
RESULT 13
AAI23408
ID AAI23408 standard; DNA; 171 BP.
XX
XX AAI23408;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #13341 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
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PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 17211; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
XX
XX Query Match 6.6%; Score 133; DB 22; Length 171;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-55;
XX Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1352 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 1411
DB 1 GGGCCAAAGTTCCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 60
QY 1412 TCAAGTCAGACGCTCGTCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 1471
DB 61 TCAAGTCAGACGCTCGTCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133
XX
RESULT 13
AAI23408
ID AAI23408 standard; DNA; 171 BP.
XX
XX AAI23408;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #13341 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
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XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
DR analyzing gene expression in human cervical epithelial cells -
XX Claim 25; SEQ ID No 13341; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
SQ
Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GGGCCAAAGTTCCCAATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 60
QY 1412 TCAAGTCAGACGTCTGGTCTTTGGTATCCTGCTGATGGAGATCGTCACTACGCCGGA 1471
DB 61 TCAAGTCAGACGTCTGGTCTTTGGTATCCTGCTGATGGAGATCGTCACTACGCCGGA 120
QY 1472 TCCTTACCAGG 1484
DB 121 TCCTTACCAGG 133
RESULT 14
AAI48728
ID AAI48728 standard; DNA; 171 BP.
AC AAI48728;
XX
DT 17-OCT-2001 (first entry)
XX Probe #17414 used to measure gene expression in human placenta sample.
DE Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX Homo sapiens.
OS
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI; 2001-48897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 25; SEQ ID No 17414; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
SQ
Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1352 GGGCCAAAGTTCCCAATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 1411
DB 1 GGGCCAAAGTTCCCAATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCTTCACCA 60
QY 1412 TCAAGTCAGACGTCTGGTCTTTGGTATCCTGCTGATGGAGATCGTCACTACGCCGGA 1471
DB 61 TCAAGTCAGACGTCTGGTCTTTGGTATCCTGCTGATGGAGATCGTCACTACGCCGGA 120
QY 1472 TCCTTACCAGG 1484
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RESULT 15
AAI09035
ID AAI09035 standard; DNA; 171 BP.
AC AAI09035;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #9026 used to measure gene expression in human breast sample.
XX Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX Homo sapiens.
OS
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
PS Claim 25; SEQ ID No 9026; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes.

The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;

Query Match 0.08; SCORE 133; DB 22;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1412 TCAAGTCAGACGTCGTCTCTTTGGTATCCTGCTGATGGAGATCGTCACCTACGSCCGGA 1471

Qy 1472 TCCCTTACCCAGG 1484

Search completed: July 4, 2003, 02:31:01
Job time : 458 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2003, 00:38:48 ; Search time 5238 Seconds
(without alignments)
11195.524 Million cell updates/sec

Title: us-10-007-010-3
Perfect score: 2015
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 2054640 seqs, 14551402878 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 28: em_un:*
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- 32: em_htg_other:*
- 33: em_htg_mus:*
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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2015	100.0	2015	6	AX334501	AX334501 Sequence
2	2015	100.0	2015	9	HUMHCKA	M16591 Human hemop
3	1606	79.7	2044	9	BC014435	BC014435 Homo sapi
4	1555	77.2	2105	9	AK026432	AK026432 Homo sapi
5	1552	77.0	1926	9	HUMHCKB	M16592 Human hemop
6	423	21.0	4507	9	HSCHKE12	X58743 H.sapiens H
7	303	15.0	111694	9	HSJ836N17	AL049539 Human DNA
8	274	13.6	333	11	G06122	G06122 human STS W
9	182	9.0	5268	9	HSCHKE69	X58741 H.sapiens H
10	157	7.8	2167	9	HSCHKE11	X58742 H.sapiens H
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12	107	5.3	1515	9	MFA320181	AJ320181 Macaca fa
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ALIGNMENTS

RESULT 1
AX334501
LOCUS AX334501
DEFINITION Sequence 5010 from Patent WO0194629.
ACCESSION AX334501
VERSION AX334501.1 GI:18125220

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

TITLE Cancer gene determination and therapeutic screening using signature


```
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Db 1321 ATTGAGGACACGAGTACACGGCTCGGGAAGGGCCCAAGTTCCTCCATCAAGTGGACAGCT 1380
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Db 1981 ATATTTAAATAAAGATATAAATCAAGTCTTAG 2015

RESULT 3
BC014435
LOCUS Homo sapiens, clone MGC:22922 IMAGE:4855747, mRNA, linear PRI 19-SEP-2001
DEFINITION Homo sapiens, clone MGC:22922 IMAGE:4855747, mRNA, complete cds.
ACCESSION BC014435
VERSION BC014435.1 GI:15680176
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2044)
Strausberg, R.
Direct Submission
Submitted (17-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 34 Row: d Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10439295.

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CDS

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VERSION 1
KEYWORDS GI:10439295
SOURCE Homo sapiens ileal mucosa cDNA to mRNA, clone_lib:kaia
clone:KAIA1741.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibehara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
JOURNAL 2 (bases 1 to 2105)
REFERENCE Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
AUTHORS Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
TITLE Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
JOURNAL University of Tokyo, Laboratory of Genome Structure Analysis, Human
AUTHORS Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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Qy	358	GCCTGTATGATTACAGGGCCATTACCGAAGAGACTCAGCTTCAGAAAGGGGACACG 417
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Qy	598	CTGGCTCTCTATGATCCGGGATAGCGACACCACTAAAGGAAGCTACTTTTGTCCGTG 657
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HUMHCKB
LOCUS

HUMHCKB 1926 bp mRNA linear PRI 08-NOV-1994

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Qy	1558	GAGCTCTACAACTCATGATCGCTGTGGAAGAACCGTCCGGAGGAGCGCCGACCTTC 1617
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Db	1984	TGGAATGGTGGATTTTGTAGTTACAGCTGTGATTTGGAAGGGAAGAACTTTCAAAATAGTAA 2043
Qy	1977	ATGAATATTTAAATAAAGATATAATGC 2005
Db	2044	ATGAATATTTAAATAAAGATATAATGC 2072

DEFINITION Human hemopoietic cell protein-tyrosine kinase (HCK) gene, complete cds, clone HK24.

ACCESSION M16592

VERSION M16592.1 GI:183913

KEYWORDS kinase; protein kinase; protein-tyrosine kinase.

SOURCE Human mitogen-stimulated leukocyte, cDNA to mRNA, clone HK24.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1926)

AUTHORS Ziegler, S.F., Marth, J.D., Lewis, D.B. and Perlmuter, R.M.

TITLE Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin

JOURNAL Mol. Cell. Biol. 7 (6), 2276-2285 (1987)

MEDLINE 87257943

PUBMED 3453117

FEATURES

Location/Qualifiers

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BASE COUNT 497 a 522 c 520 g 387 t

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Query Match 77.0%; Score 1552; DB 9; Length 1926;

Best Local Similarity 100.0%; Pred. No. 0;

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DB 145 AGCCACACTGTCTGTAGTGGCGGATCCACATCCACATCCAGCGGGGCCCTAAT 204
QY 298 AGCCACACACACACACACAGGAATCAGGAGGCGAGCTCTGAGGACATCATCGTGGTT 357
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DB 205 AGCCACACACACACACAGGAATCAGGAGGCGAGCTCTGAGGACATCATCGTGGTT 264
QY 358 GCCCTGTATGATTACGAGGCCATTCCACACGAAGACCTTCAGCTTCCAGAGGGGGACAG 417
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DB 265 GCCCTGTATGATTACGAGGCCATTCCACACGAAGACCTTCAGCTTCCAGAGGGGGACAG 324
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QY 478 GAGGCTACATCCCAAGCAATATCTGCCCGCTTGACTCTCTGGACACAGAGAGTGG 537
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RESULT 6
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LOCUS             HSHCKE12
DEFINITION       H sapiens HCK gene for tyrosine kinase (PK), exon 12.
ACCESSION        X58743 X59743
VERSION          X58743.1 GI:32044
KEYWORDS         proto-oncogene; src family; T-cell receptor alpha-chain; Tyrosine
SOURCE           HCK
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 4507)
AUTHORS          Hradetzky,D., Strebhardt,K. and Rubsamen-Waigmann,H.
TITLE            The genomic locus of the human hemopoietic-specific cell protein
                tyrosine kinase (PK)-encoding gene (HCK) confirms conservation of
                exon-intron structure among human PKs of the src family
                Gene 113 (2), 275-280 (1992)
JOURNAL          92241680
MEDLINE          1572549
PUBMED           1572549
REFERENCE        2 (bases 1 to 4507)
AUTHORS          Hradetzky,D.
TITLE            Direct Submission
JOURNAL          Submitted (14-JUN-1991) D. Hradetzky, Chemotherapeutisches
                Forschungsinstitut, Georg-Speyer-Haus, Paul Ehrlich Str 42-44, 6000
                Frankfurt 70, Federal Republic of Germany
                See also X58736-X58740, X58744-X58769
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Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1541 CAGAGAACTGCCAGAGGAGGCTCTACAAATCATGATGCGCTGCTGGAACCAACCGTCCGG 1600
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Db 4284 CTTTCAAAATAGTGAATGAATATTATAAATAAAGATATAAATGC 4328

RESULT 7
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LOCUS             HSHJ836N17
DEFINITION       Human DNA sequence from clone RP5-836N17 on chromosome
                20q11.1-11.21 Contains part of the HCK (hemopoietic cell kinase)
                gene, the KIAA0255 gene, a ribosomal protein L30 pseudogene, ESTs,
                STSS, GSSS and Cpg Islands, complete sequence.
                AL049539
                HTG: Cpg island; HCK; hemopoietic; KIAA0255; kinase; RPL30.
                human.
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                Sehra,H.
                Direct Submission
                Submitted (26-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
                CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
                requests: clonerequest@sanger.ac.uk
                On Nov 21, 1999 this sequence version replaced gi:6433925.
                During sequence assembly data is compared from overlapping clones.
                Where differences are found these are annotated as variations .
                together with a note of the overlapping clone name. Note that the
                variation annotation may not be found in the sequence submission
                corresponding to the overlapping clone, as we submit sequences with
                only a small overlap as described above.
                The following abbreviations are used to associate primary accession
                numbers given in the feature table with their source databases:
                Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WormPEP; Information
                on the WormPEP database can be found at
                http://www.sanger.ac.uk/projects/c_elegans/wormpep
                The entire insert of clone RP5-836N17 The true left end of clone
                RP11-392M18 is at 77067 in this sequence. This sequence was
                generated from part of bacterial clone contigs of human chromosome
                20, constructed by the Sanger Centre Chromosome 20 Mapping Group.
                Further information can be found at
                http://www.sanger.ac.uk/HGP/Chr20
                This sequence was finished as follows unless otherwise noted: all
                regions were either double-stranded or sequenced with an alternate
                chemistry or covered by high quality data (i.e., phred quality >=
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30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-836N17 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.

FEATURES

source

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 /clone_lib="RPCI-5"
 1..62

repeat_region /note="AluJ/FLAM repeat: matches 1..62 of consensus"

repeat_region 73..173

/note="L2 repeat: matches 2597..2709 of consensus"

repeat_region 243..302

/note="15 copies 4 mer catc 98% conserved"

repeat_region 601..898

/note="AluSq repeat: matches 1..295 of consensus"

repeat_region 1188..1345

/note="MER5A repeat: matches 1..185 of consensus"

repeat_region 1364..1668

/note="AluSx repeat: matches 1..307 of consensus"

repeat_region 2074..2381

/note="AluSp repeat: matches 3..313 of consensus"

repeat_region 2583..2904

/note="AluY repeat: matches 1..311 of consensus"

repeat_region 2993..3134

/note="MIR repeat: matches 2..143 of consensus"

repeat_region 3135..3439

/note="AluSx repeat: matches 1..305 of consensus"

repeat_region 3440..3503

/note="MIR repeat: matches 143..206 of consensus"

repeat_region 3491..3594

/note="MIR repeat: matches 60..164 of consensus"

repeat_region 3866..4024

/note="MER69 repeat: matches 66..236 of consensus"

repeat_region 4033..4126

/note="MER69 repeat: matches 2422..2510 of consensus"

misc_feature complement(4261..4710)

/note="match: GSS: Em:AQ339627"

gene 4334..26412

/gene="HCK"

join(<4334..4437,8454..8603,8951..9103,11188..11367,

13128..13204,18423..18576,23564..23695,25877..26412)

/gene="HCK"

/product="dJ836N17.1 (hemopoietic cell kinase)"

/note="match: CDNAS: Em:J03023 Em:M83666 Em:S74141

Em:X62345 Em:X00487 Em:M12056 Em:M57697 Em:M36881

Em:M57696 Em:U23852 Em:M30903 Em:U01349 Em:X03533

Em:L14823 Em:X52191 Em:U70324 Em:M19722 Em:M17031

Em:X15345 Em:U35365 Em:M79321 Em:J03579 Em:AF000302

Em:M64608 Em:AF000301 Em:X13529 Em:AF000300 Em:X12461

Em:M23422 Em:L14951 Em:X54970 Em:X54971 Em:M14676

Em:M27266 Em:AF130457 Em:X52822 Em:S76617 Em:M16440

Em:M16592 Em:M16591 Em:M16038 Em:M14333 Em:L14782

Em:AF081803 Em:X05027 Em:X57018 Em:X13207 Em:Z33998

Em:U07236 Em:X67786 Em:X67677 Em:M24704

match: ESTs: Em:AA763708 Em:AA149096 Em:W87315 Em:AI912730

Em:AI220607 Em:AI572095"

/evidence="not_experimental"

join(<4334..4437,8454..8603,8951..9103,11188..11367,

13128..13204,18423..18576,23564..23695,25877..26079)

/gene="HCK"

/note="Continues in Em:AL353092 as dJ180113.1

match: proteins: Sw:P06239 Sw:P06240 Sw:P08103 Sw:P50545

Tr:Q13084 Sw:P42683 Sw:P08631 Sw:Q07014 Sw:P07948"

/codon_start=2

/evidence="not_experimental"
 /product="dJ836N17.1 (hemopoietic cell kinase)"
 /protein_id="CAB75606.1"
 /db_xref="GI:7018398"
 /db_xref="SPTREMBL:Q9NUM4"
 /translation="WFFGIGSRKDAEROLLAPGNMLGSFMTRDSETTKGYSLSVROY
 DPQGDYTKHYKIRITLDNGFYIISPRSTFSLQELVDHYKKGNDGLCQKLSVPCMSK
 POKPEKDAWEIPRESLKLKGLAGQGFYVMATYKNTKHTVAVTKMPPGSMSEAF
 AEANVMKTLQHDKLVKHAVTKPIYIITFMAKGSLLDLKSDGSKOPLPKLIDF
 SAQIAEGMAFTEORNYIHRDLRAANILSVCKIADFGIARVIDENYFARGAKF
 PIKWTAPEINFGSTIKSDVMSFGILLMEIYTYGRIPYPCGMSPEVIRALERGYRMP
 RPENCPEELINIMRCWKNRPERTFEIIQSVLDDFTIATESIQQQP"
 4751..5056
 /note="AluSc repeat: matches 1..306 of consensus"
 5059..5348
 /note="AluJb repeat: matches 24..295 of consensus"
 5406..5666
 /note="AluJo repeat: matches 41..300 of consensus"
 complement(5985..6147)
 /note="match: STS: Em:AA443921"
 6602..6796
 /note="MIR repeat: matches 10..205 of consensus"
 6860..6919
 /note="MIR repeat: matches 187..242 of consensus"
 6920..7219
 /note="AluSx repeat: matches 1..300 of consensus"
 7220..7328
 /note="MIR repeat: matches 64..187 of consensus"
 7378..7456
 /note="MADE1 repeat: matches 2..80 of consensus"
 7461..7926
 /note="MLTLD repeat: matches 1..505 of consensus"
 8095..8311
 /note="MIR repeat: matches 35..261 of consensus"
 9492..9524
 /note="L2 repeat: matches 2652..2686 of consensus"
 9791..10099
 /note="AluSx repeat: matches 1..308 of consensus"
 10223..10555
 /note="L2 repeat: matches 2141..2482 of consensus"
 10576..10867
 /note="AluY repeat: matches 12..303 of consensus"
 10880..11054
 /note="MIR repeat: matches 21..188 of consensus"
 11862..12205
 /note="AluJo repeat: matches 257..302 of consensus"
 12206..12501
 /note="AluY repeat: matches 1..295 of consensus"
 12502..12764
 /note="AluJo repeat: matches 1..257 of consensus"
 13048..13092
 /note="MADE1 repeat: matches 36..79 of consensus"
 complement(13162..13462)
 /note="match: STS: Em:HS180113S"
 complement(13162..13412)
 /note="match: STS: Em:AL031189"
 13302..13417
 /note="MIR repeat: matches 151..262 of consensus"
 13418..13810
 /note="MLTLH repeat: matches 99..540 of consensus"
 13835..13922
 /note="MIR repeat: matches 101..182 of consensus"
 13921..13981
 /note="MIR repeat: matches 76..137 of consensus"
 13951..14131
 /note="L2 repeat: matches 2505..2726 of consensus"
 14285..14527
 /note="L2 repeat: matches 2300..2551 of consensus"
 15366..15471
 /note="MIR repeat: matches 23..135 of consensus"
 15483..15707
 /note="MIR repeat: matches 1..256 of consensus"
 15855..16037

CDS

```
/note="MIR repeat: matches 12. .193 of consensus"
16288. .16567
/note="AluJo repeat: matches 5. .312 of consensus"
16872. .16920
/note="MIR repeat: matches 125. .173 of consensus"
17077. .17497
/note="L2 repeat: matches 2098. .2595 of consensus"
17498. .17804
/note="Alusx repeat: matches 1. .307 of consensus"
complement(17780. .18196)
/note="match: GSS: Em:AQ590401"
17805. .17925
/note="L2 repeat: matches 2595. .2710 of consensus"
complement(17926. .18196)
/note="match: GSS: Em:AQ590401"

Query Match 15.0%; Score 303; DB 9; Length 111694;
Best Local Similarity 99.4%; Pred. No. 1e-162;
Matches 523; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1481 CAGGGATGTCAAAACCTGAAGTATCGAGCTCTGGAGCGTGGATACCGGATCCCTCGCC 1540
|||||
Db 25874 CAGGGATGTCAAAACCTGAAGTATCGAGCTCTGGAGCGTGGATACCGGATCCCTCGCC 25933
|||||
QY 1541 CAGAGAACTGCCAGAGAGCTCTACAACATCATGATCGCTGCGAAACCGTCGCG 1600
|||||
Db 25934 CAGAGAACTGCCAGAGAGCTCTACAACATCATGATCGCTGCGAAACCGTCGCG 25993
|||||
QY 1601 AGGAGCGCGCCACCTTCGAATACATCCAGAGTGTGCTGGATGACTTCTACACGGCCACAG 1660
|||||
Db 25994 AGGAGCGCGCCACCTTCGAATACATCCAGAGTGTGCTGGATGACTTCTACACGGCCACAG 26053
|||||
QY 1661 AGACCCAGTACCAACAGACGCCATGATAGGAGGACAGGGCAGGG-CAGGGGGTGCCTCA 1719
|||||
Db 26054 AGACCCAGTACCAACAGACGCCATGATAGGAGGACAGGGCAGGGCAGGGGGTGCCTCA 26113
|||||
QY 1720 GGTGGTGGCTCGAGGGGCTCCAGCACCATCCGCCAGGCCACACACCCCTTCTTCTACTC 1779
|||||
Db 26114 GGTGGTGGCTCGAGGGGCTCCAGCACCATCCGCCAGGCCACACACCCCTTCTTCTACTC 26173
|||||
QY 1780 CCAGACACCCACCCCTCGCTTCAGCCACAGTTTCTCATCTGTCCAGTGGGTAGGTGGAC 1839
|||||
Db 26174 CCAGACACCCACCCCTCGCTTCAGCCACAGTTTCTCATCTGTCCAGTGGGTAGGTGGAC 26233
|||||
QY 1840 TGGAAATCTCTTTTTCACCTTTCGCAATCCACAATCTGACATCTCAGGAAGCCCCCAG 1899
|||||
Db 26234 TGGAAATCTCTTTTTCACCTTTCGCAATCCACAATCTGACATCTCAGGAAGCCCCCAG 26293
|||||
QY 1900 TTGATATTTCTATTTCTTGGAAATGGTTGGATTTTGTACAGCTGTGATTTTGAAGGAA 1959
|||||
Db 26294 TTGATATTTCTATTTCTTGGAAATGGTTGGATTTTGTACAGCTGTGATTTTGAAGGAA 26353
|||||
QY 1960 ACTTTCAAAATAGTGAATGAATTAATTAATAAAGATATAAATGC 2005
|||||
Db 26354 ACTTTCAAAATAGTGAATGAATTAATTAATAAAGATATAAATGC 26399
|||||

RESULT 8
G06122 333 bp DNA linear STS 19-OCT-1995
LOCUS human STS WI-7020, sequence tagged site.
DEFINITION G06122
ACCESSION G06122
VERSION G06122.1 GI:859367
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STSS derived from sequences in dbEST and the Unigene collection.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 333)
REFERENCE
AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
```

JOURNAL
COMMENT

Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TAGGAGGACACGAGGCAG
Primer B: TGGTAAAGACTTTGGCATTTATATC
STS size: 333
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3

Prepared with primer pairs derived from X58743 -- Unigene.

FEATURES
Source

1..333
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="734_E.7; 908_C.6; 768_C.11; (808,809)_(G.A)_(1,6)"

STS
1..333

primer_bind
1..18

primer_bind complement(309..333)

BASE COUNT 87 a 83 c 77 g 86 t

ORIGIN

Query Match 13.6%; Score 274; DB 11; Length 333;

Best Local Similarity 100.0%; Pred. No. 4.8e-146;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1732 AGGTGGCTCCAGCACCATCCGCCAGGCGCCACACCCCTTCTTACTCCGAGACACCCAC 1791

Db 46 AAGTGGCTCCAGCACCATCCGCCAGGCGCCACACCCCTTCTTACTCCGAGACACCCAC 105

QY 1792 CCTCGCTTCAGCCACAGTTTCTCATCTGTCCAGTGGGTAGGTGGAGTGGAAATCTCT 1851

Db 106 CCTCGCTTCAGCCACAGTTTCTCATCTGTCCAGTGGGTAGGTGGAGTGGAAATCTCT 165

QY 1852 TTTTGACTCTTGCATCCACAATCTGACATCTCAGGAAGCCCCCAAGTTGATATTTCTA 1911

Db 166 TTTTGACTCTTGCATCCACAATCTGACATCTCAGGAAGCCCCCAAGTTGATATTTCTA 225

QY 1912 TTTTCTGGAATGGTTGGATTTTACTTACAGCTGTGATTTGGAAGGAACTTTCAAATA 1971

Db 226 TTTTCTGGAATGGTTGGATTTTACTTACAGCTGTGATTTGGAAGGAACTTTCAAATA 285

QY 1972 GTGAATCAATATTTAAATAAAGATATAAATGC 2005

Db 286 GTGAATCAATATTTAAATAAAGATATAAATGC 319

RESULT 9

HSCKE69

LOCUS

HSCKE69 5268 bp DNA linear PRI 27-AUG-1999


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/db_xref="taxon:9606"
/chromosome="20"
/map="q11-12"
/clone="D640 H"
/tissue_type="spleen"
/clone_lib="genomic; TS48"
/dev_stage="adult"
<1..15
/intron
/number=9
16..1065
/gene="HCK"
16..169
/gene="HCK"
/number=10
/usedin=X58741:HCK_cds
/usedin=X58741:HCK_mRNA
170..933
/gene="HCK"
/number=10
203..430
/note="ALU repeat V"
934..1065
/gene="HCK"
/number=11
/usedin=X58741:HCK_cds
/usedin=X58741:HCK_mRNA
1066..>2167
/number=11
1281..1592
/note="ALU repeat VI"
1835..2167
/note="ALU repeat VII"
BASE COUNT 477 a 626 c 485 g 579 t
ORIGIN
Query Match 7.88; Score 157; DB 9; Length 2167;
Best Local Similarity 100.0%; Pred. No. 2.4e-78;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1196 AGATTGCGAAGGATGGCTTCATCGAGCAGAGGAACATACCCAGAGACTCCGAG 1255
Db 14 AGATTGCGAAGGATGGCTTCATCGAGCAGAGGAACATACCCAGAGACTCCGAG 73
Qy 1256 CTGCCACATCTGGTCTGTCATCCCTGCTGTGTAGATTGCTGACTTTGGCTGGCCC 1315
Db 74 CTGCCACATCTGGTCTGTCATCCCTGCTGTGTAGATTGCTGACTTTGGCTGGCCC 133
Qy 1316 GGGTCATTGAGGACAACGAGTACAGCTCGGGAAG 1352
Db 134 GGGTCATTGAGGACAACGAGTACAGCTCGGGAAG 170

RESULT 11
AL353092 25010 bp DNA linear PRI 11-FEB-2001
LOCUS Human DNA sequence from clone RPI-180113 on chromosome 20 contains
DEFINITION 5' end of the HCK gene for hemopoietic cell kinase (protein
tyrosine kinase), contains ESTs, STSS, GSSs and a CpG island,
complete sequence.
ACCESSION AL353092
VERSION AL353092.6 GI:9650539
KEYWORDS HTG; CpG island; HCK; tyrosine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25010)
AUTHORS Almeida, J.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Aug 1, 2000 this sequence version replaced gi:9187765.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
IMPORTANT: This sequence is not the entire insert of clone
RPI-180113 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP5-836N17 is at 24911 in this sequence.
The true right end of clone RPI-310013 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RPI-180113 is from
the library RPCI-1 constructed by the group of Pieter de Jong. For
further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
Location/Qualifiers
1..25010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RPI-180113"
/clone_lib="RPCI-1"
1..43
/note="AluJo/FLAM repeat: matches 76..118 of consensus"
complement(39..567)
/note="match: GSS: Em:AQ386884"
58..175
/note="5S repeat: matches 1..119 of consensus"
265..455
/note="MER20 repeat: matches 26..218 of consensus"
510..586
/note="L2 repeat: matches 1966..2045 of consensus"
692..906
/note="match: GSS: Em:AQ486790"
772..843
/note="2 copies 36 mer 93% conserved"
1576..2453
/note="CpG island"
/evidence="not_experimental"
1846..24191
/gene="HCK"
Join(1846..1956,21132..21252,22789..22831,23186..23288,
24093..>24191)
/gene="HCK"
/product="dJ180113.1 (hemopoietic cell kinase)"
/note="match: CDNAS: Em:M15591 Em:X62345 Em:S74141
Em:J03023 Em:M16592 Em:M83666 Em:Y00487 Em:X60380
Em:J03579 Em:X67786 Em:AF000300 Em:AF000301 Em:AF000302
Em:M17031 Em:X52822 Em:X57018 Em:X15345 Em:M27454
Em:X57250 Em:X57684 Em:M85043 Em:M19722
match: ESTs: Em:AW307786"
/evidence="not_experimental"
complement(2102..2519)
/note="match: GSS: Em:AQ382576"
complement(2108..2557)
/note="match: GSS: Em:AQ461389"
complement(2196..2570)
misc_feature
misc_feature
misc_feature
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gene
CDS
1. .1515
/gene="hck"
1. .1515
/gene="hck"
/function="tyrosine kinase"
/codon_start=1
/product="hck protein"
/protein_id="CAC44031.1"
/db_xref="GI:14627116"
/translation="MGCMKSKFLQAGNFTSKTSSANPCPVYVDPDTSTIKPGPNS
NNRTGICGEGSDIIVVALDYEAIIHEDLSFORGDQMVLEESGEWNKARSLATRK
EGVPSNYVARVDSLETEWFFKISRDAERQLLAPGNMLGSEMRDSETTKGSYSL
SVRDYPRGDDYVKKIKIRTLNGFEYISPRSTFYLQELVDHYKKGSDGLCKLSVP
CVSSKPKWEKDAWIPRESLKKLKGAGQFGEVMAKNGSLLDVAVKTKMKGMS
VEAFIAELMLTQHDKLVLKLVAVVTEPIYIITEFMAKGLSLDLFLAKSDGSKQPLP
KLDFSAQIAEGMAFTEQRNYIHRDLRAANILSVASLCKIADFLARIENDEYTA
EGAKFKIKTAQPAINFSGSTIKSDWSFGLIMEIVTVGRIPYPCMSNPEVIRALER
GYMRPENCPEELYNIMRCKNRPETFEYIQSVLDDFTYATESQYQQP"
BASE COUNT 388 a 424 c 419 g 284 t
ORIGIN
Query Match 5.3%; Score 107; DB 9; Length 1515;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 580 CTGGCTCCCGGCAACATGCTGGGCTCCTTCATGATCCGGGATAGCGAGACCCTAAAGGA 639
|||||
Db 409 CTGGCTCCCGGCAACATGCTGGGCTCCTTCATGATCCGGGATAGCGAGACCCTAAAGGA 468
QY 640 AGCTACTCTTTGTCCTGGGAGACTACGACCCCTCGCGAGGGAGATAC 686
|||||
Db 469 AGCTACTCTTTGTCCTGGGAGACTACGACCCCTCGCGAGGGAGATAC 515
RESULT 13
G25924
LOCUS human STS EST50744, 366 bp DNA linear STS 02-JUN-1996
DEFINITION human STS EST50744, sequence tagged site.
ACCESSION G25924
VERSION G25924.1 GI:1348156
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 366)
AUTHORS Hudson, T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped STSs
JOURNAL Unpublished (1995)
COMMENT Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
Primer A: GATCCGAGCTCTGGAGCG
Primer B: CCGGTAGAGTCATCCAGC
STS size: 150
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pM

dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul
Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3
Derived from dbEST (genbank accession D20116).
FEATURES
source Location/Qualifiers
1..366
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="180.1 cR from top of Chr20 linkage group"
STS
1..150
primer_bind 1..18
primer_bind complement(131..150) 73 t 18 others
BASE COUNT 83 a 95 c 97 g 73 t 18 others
ORIGIN
Query Match 4.1%; Score 82; DB 11; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.3e-35;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1613 CTTTGAATACATCCAGAGTGTGCTGGATGACTTCTACAGGCCACAGAGCCAGTACC 1672
|||||
Db 109 CTTTGAATACATCCAGAGTGTGCTGGATGACTTCTACAGGCCACAGAGCCAGTACC 168
QY 1673 AACAGCAGCCATGATAGGAGG 1694
|||||
Db 169 AACAGCAGCCATGATAGGAGG 190
RESULT 14
HUMHCK
LOCUS Human hemopoietic cell kinase (HCK) gene, exon 1.
DEFINITION Human hemopoietic cell kinase (HCK) gene, exon 1.
ACCESSION M73233
VERSION M73233.1 GI:485365
KEYWORDS hemopoietic cell kinase.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 958)
AUTHORS Lichtenberg, U., Quintrell, N. and Bishop, J.M.
TITLE Human protein-tyrosine kinase gene HCK: expression and structural analysis of the promoter region
JOURNAL Oncogene 7 (5), 849-858 (1992)
MEDLINE 92237010
PUBMED 1373873
FEATURES
source Location/Qualifiers
1..958
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20q11-q12"
/cell_type="lymphocyte"
1..663
5'UTR 664..958
gene /gene="HCK"
exon 664..807
/product="hemopoietic cell kinase"
/note="G00-119-303"
/number=1
808..958
intron /gene="HCK"
/note="G00-119-303"
BASE COUNT 177 a 219 c 379 g 183 t
ORIGIN

Query Match	3.8%; Score 77; DB 9; Length 958;
Best Local Similarity	100.08; Pred. No. 4.3e-32;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	89 ACCTCAGGGCTGCCGAGCTGGGGGGCGCTCAAGCTCGGAGGATCGGGGCTGCCCGCA 148
Db	728 ACCTCAGGGCTGCCGAGCTGGGGGGCGCTCAAGCTCGGAGGATCGGGGCTGCCCGCA 787
QY	149 GACGAGGAGCGGGCGCC 165
Db	788 GACGAGGAGCGGGCGCC 804
RESULT 15	
AB071605	10348 bp mRNA linear PRI 02-AUG-2002
LOCUS	AB071605 Homo sapiens mRNA for HECT domain protein LASU1, complete cds.
DEFINITION	AB071605
ACCESSION	AB071605.1 GI:22090625
VERSION	
KEYWORDS	Homo sapiens fetus brain cDNA to mRNA.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Gu,J., Ren,K., Dubner,R. and Iadarola,M.J. Cloning of a DNA binding protein that is a tyrosine kinase substrate and recognizes an upstream initiator-like sequence in the promoter of the preprodynorphin gene Brain Res. Mol. Brain Res. 24 (1-4), 77-88 (1994) 95058008 7968380
REFERENCE	2 Gu,J., Dubner,R., Fornace,J.A. and Iadarola,M. UREB1, a tyrosine phosphorylated nuclear protein, inhibits p53 transactivation Oncogene 16, 2175-2178 (1995)
JOURNAL	3 Miyazaki,K., Okamoto,Y., Sakamoto,M., Kato,C., Ozaki,T., Watanabe,K. and Nakagawa,A. Homo sapiens LASU1 (large structure of UREB1) mRNA, complete cds Unpublished
REFERENCE	4 (bases 1 to 10348) Nakagawa,A. and Miyazaki,K. Direct Submission Submitted (16-SEP-2001) Akira Nakagawa, Chiba Cancer Center Research Institute, Division of Biochemistry; 666-2 Nitona, Chuoh-ku Chiba, Chiba 260-8717, Japan (E-mail: akiranak@chiba-cc.pref.chiba.jp, Tel:81-43-264-3431, Fax:81-43-265-4459)
JOURNAL	Location/Qualifiers
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 Job time : 5242 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2003, 00:36:13 ; Search time 456 Seconds
(without alignments)
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Title: US-10-007-010-3
Perfect score: 2015
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2015	100.0	2015	24	ABK83939 Human CDNA differe
2	2015	100.0	2015	24	ABL66673 Lung cancer relate
3	1552	77.0	1926	24	ABK83940 Human CDNA differe
4	183	9.1	183	24	ABL61214 Human nucleotide f
5	181	9.0	1416	24	ABL61215 Rat/human fusion c
6	181	9.0	1542	24	ABL61216 Rat/human fusion c
7	169	8.4	369	16	AA119957 Human gene signatu
8	133	6.6	171	22	ABA50558 Human breast cell
9	133	6.6	171	22	ABA68516 Human foetal liver

10	133	6.6	171	22	ABA35497	Probe #13963 for g
11	133	6.6	171	22	AAK16884	Human brain expres
12	133	6.6	171	22	AAK42654	Human bone marrow
13	133	6.6	171	22	AAI23408	Probe #13341 for g
14	133	6.6	171	22	AAI48728	Probe #17414 used
15	133	6.6	171	22	AAI09035	Probe #9026 used t
16	133	6.6	171	22	ABSI6706	Human genome-deriv
17	133	5.6	415	22	ABA45430	Human breast cell
18	113	5.6	415	22	ABA55928	Human foetal liver
19	113	5.6	415	22	ABA25595	Probe #4061 for ge
20	113	5.6	415	22	AAK04142	Human brain expres
21	113	5.6	415	22	AAK29623	Human bone marrow
22	113	5.6	415	22	AAI14202	Probe #4135 for ge
23	113	5.6	415	22	AAI35583	Probe #4269 used t
24	113	5.6	415	22	AAI04039	Probe #4030 used t
25	113	5.6	415	24	ABS04179	Human genome-deriv
26	112	5.6	1592	20	AAI27241	Human secreted pro
27	78	3.9	409	22	AAH99174	Human protein enco
28	77	3.8	334	21	AAA52650	Eosinophil activat
29	68	3.4	1911	24	AAK63704	Rat sequence diffe
30	66	3.3	274	22	AAK68573	Human immune/haema
31	65	3.2	1926	24	AAK83940	Human CDNA differe
32	31	1.5	31	22	AAI30734	Human single nucle
33	31	1.5	31	22	AAI30735	Human single nucle
34	31	1.5	31	22	AAI30736	Human single nucle
35	31	1.5	31	22	AAI30737	Human single nucle
36	31	1.5	31	22	AAI30738	Human single nucle
37	28	1.4	2298	24	ABK83935	Human CDNA differe
38	27	1.3	33	22	AAH41498	Human tyrosine kin
39	26	1.3	32	22	AAH41491	Human tyrosine kin
40	26	1.3	32	22	AAH41492	Human tyrosine kin
41	26	1.3	1602	14	AAO46687	Chicken pp60 c-src
42	26	1.3	1759	21	AAI29700	Wild-type chicken
43	26	1.3	1759	22	AAH28357	Nucleotide sequenc
44	25	1.2	32	22	AAH41501	Human tyrosine kin
45	25	1.2	51	23	ABL00375	Human silent nonco

ALIGNMENTS

RESULT 1

ABK83939

ID ABK83939 standard; cDNA; 2015 BP.

XX

AC ABK83939;

XX

14-AUG-2002 (first entry)

XX

Human CDNA differentially expressed in granulocytic cells #510.

XX

Human; ss; granulocytic cell; DNA chip; bacterial infection;

XX viral infection; parasitic infection; protozoal infection;

XX fungal infection; sterile inflammatory disease; psoriasis;

XX rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

XX cardiac reperfusion injury; renal reperfusion injury; ARDS;

XX adult respiratory distress syndrome; inflammatory bowel disease;

XX Crohn's disease; ulcerative colitis; periodontal disease;

XX granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX

WO200228999-A2.

XX

11-APR-2002.

XX

03-OCT-2001; 2001WO-US30821.

XX

03-OCT-2000; 2000US-237189P.

XX

(GENE-) GENE LOGIC INC.

XX

Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX

PI

[illegible]

RESULT. T 2.

RESUL 2
ABL66673

ABL66673
ID ABL66673 standard; DNA: 2015 BP.

XX
XX

AC ABL66673;

XX

DT 15-MAY-2002 (first entry)

XX
DE Lung cancer related gene sequence SEQ ID NO:5010.

XX

KW Human; cancer; colon; breast; ovary; oesophagus; kidney: thyroid; thyroid;

KW stomach;

KW cytostati

KW gene; ds.

XX

OS Homo sapi

[illegible]

PN WO2001946

XX
13-DEC-30

PD 13-DEC-20
yy

XX
DE 30-MAY-70

PF 30-MAY-20 YY

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PR	01-NOV-2000;	2000US-244867P.
PR	01-NOV-2000;	2000US-244868P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;

WPI: 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene

Claim 1: SEO ID 5010: 44pp: English:

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.

Sequence 2015 BP: 512 A: 540 C: 580 G: 383 T: 0 other:

Query Match 100.0%: score 2015: DB 24: Length 2015:

Query match	100.00%	Score 2015,
Best Local Similarity	100.00%	Pred. No. 0:

Best Local Similarity 100.0%, Fied: NO: 0
Matches 2015: Conservative 0: Mismatches

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10/7	SALES	75.00	100.00
10/8	PAYROLL	25.00	75.00
10/9	RENT	50.00	25.00
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DB			
1141	AAAAGTGATGAGGCGACGACAGCAGCCATTCGCCAAAAGCTCATTGACATCTCTCAGCCCCAGATT	1200	
QY	1201	GCAGAAAGCATGGCTTTCATCTCGAGCAGAGAACTACATCCACCGAGACCTTCCGAGCTGCC	1260
DB			
1201	GCAGAGGCATGGCTTTCATCTCGAGCAGAGAACTACATCCACCGAGACCTTCCGAGCTGCC	1260	
QY	1261	AACATCTTGGTCTCTGCATCCCTGGTGTGAAGATTGCTGACATTTGGCCTGGCCCGGGTC	1320
DB			
1261	AACATCTTGGTCTCTGCATCCCTGGTGTGAAGATTGCTGACATTTGGCCTGGCCCGGGTC	1320	
QY	1321	ATTGAGACACGAGTAGTACAGCGTCTGGGAGGGGCCAAGTTCCTCCATCAAGTGGACAGCT	1380
DB			
1321	ATTGAGACACGAGTAGTACAGCGTCTGGGAGGGGCCAAGTTCCTCCATCAAGTGGACAGCT	1380	
QY	1381	CCTGAAGCCATCAACTTTGGCTCCTTCCACCATCAAGTCAAGCTCTGGTCTTTGGTATC	1440
DB			
1381	CCTGAAGCCATCAACTTTGGCTCCTTCCACCATCAAGTCAAGCTCTGGTCTTTGGTATC	1440	
QY	1441	CTGCTGATGGAGATGTCCTACCTAGGCGCCGATCCCTTACCCAGGATGTCAAACCTCGAA	1500
DB			
1441	CTGCTGATGGAGATGTCCTACCTAGGCGCCGATCCCTTACCCAGGATGTCAAACCTCGAA	1500	
QY	1501	GTGATCCGAGCTCTGGAGCGTGGATACCGGATGCCTCGCCACAGAGACTGCCCAGAGGAG	1560
DB			
1501	GTGATCCGAGCTCTGGAGCGTGGATACCGGATGCCTCGCCACAGAGACTGCCCAGAGGAG	1560	
QY	1561	CTCTACAAACATCATGATGCGCTGCTGGAAAAACCGTCCGGAGGAGCGCGACTTTCGAA	1620
DB			
1561	CTCTACAAACATCATGATGCGCTGCTGGAAAAACCGTCCGGAGGAGCGCGACTTTCGAA	1620	
QY	1621	TACATCCAGAGTGTCTGATGATCTTACACGGCCACAGAGAGCCAGTACCAACAGCAG	1680
DB			
1621	TACATCCAGAGTGTCTGATGATCTTACACGGCCACAGAGAGCCAGTACCAACAGCAG	1680	
QY	1681	CCATGATAGGAGGACACGAGGAGGCGGGGTGCCAGGTGGTGGCTCGAAGGTGGCT	1740
DB			
1681	CCATGATAGGAGGACACGAGGAGGCGGGGTGCCAGGTGGTGGCTCGAAGGTGGCT	1740	
QY	1741	CCAGCACATCTCGCCAGGGGCCACACCCCTTCTACTCCAGACACCCACCTCCGCTTC	1800
DB			
1741	CCAGCACATCTCGCCAGGGGCCACACCCCTTCTACTCCAGACACCCACCTCCGCTTC	1800	
QY	1801	AGCCACAGTTTCTCATCTCTGCAGTGGGTAGGCTGGAAAAATCTCTTTTTGACTC	1860
DB			
1801	AGCCACAGTTTCTCATCTCTGCAGTGGGTAGGCTGGAAAAATCTCTTTTTGACTC	1860	
QY	1861	TTGCAATCCCAATCTGACATCTCAGGAGCCCCCAAGTTTGATATTCTATTTCCTGGA	1920
DB			
1861	TTGCAATCCCAATCTGACATCTCAGGAGCCCCCAAGTTTGATATTCTATTTCCTGGA	1920	
QY	1921	ATGTTTGGATTTTAGTTTACAGCTGTGATTTGGAGGGAACCTTTCAAAATAGTGAATGA	1980
DB			
1921	ATGTTTGGATTTTAGTTTACAGCTGTGATTTGGAGGGAACCTTTCAAAATAGTGAATGA	1980	
QY	1981	ATATTTAAATAAAGATATAAATCGAAGCTTTACG	2015
DB			
1981	ATATTTAAATAAAGATATAAATCGAAGCTTTACG	2015	

RESULT 3
ABK83940
ID - ABK83940 standard; cDNA; 1926 BP.
XX
AC ABK83940;
XX
DT 14-AUG-2002 (first entry)
XX

DE Human cDNA differentially expressed in granulocytic cells #511.
XX Human; ss: granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX Homo sapiens.
OS
XX WO200228999-A2.
PN
XX 11-APR-2002.
PD
XX 03-OCT-2001; 2001WO-US30821.
PF
XX 03-OCT-2000; 2000US-237189P.
PR
XX (GENE-) GENE LOGIC INC.
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
PI WPI; 2002-435328/46.
DR
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 511; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GCA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1926 BP; 497 A; 522 C; 520 G; 387 T; 0 other;

	Query Match	77.0%	Score 1552;	DB 24;	Length 1926;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1552;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	178	ATGAAGTCCCAAGTTCCTCCAGGTCGGAGGCAATACATTTCTCAAAAACTGAAACCCAGCGCC	237		
Db	85	ATGAAGTCCCAAGTTCCTCCAGGTCGGAGGCAATACATTTCTCAAAAACTGAAACCCAGCGCC	144		
Qy	238	AGCCACACTGCTCTGTGTAGTTCAGTTCGGGATCCACATCCACCATCAAGCCGGGGCTTAAT	297		
Db	145	AGCCACACTGCTCTGTGTAGTTCAGTTCGGGATCCACATCCACCATCAAGCCGGGGCTTAAT	204		
Qy	298	AGCCACACAGCAACACACACAGGAATCAGGAGGAGGCTCTGAGGACATCATCTGTGTT	357		
Db	205	AGCCACACAGCAACACACACAGGAATCAGGAGGAGGCTCTGAGGACATCATCTGTGTT	264		
Qy	358	GCCTGTATGATTTACGAGGCCATTTACCACGAGACCTCAGCTTCAGAGGGGGACACAG	417		
Db	265	GCCTGTATGATTTACGAGGCCATTTACCACGAGACCTCAGCTTCAGAGGGGGACACAG	324		
Qy	418	ATGTTGGTCTAGAGGAATCCGGGGAGTGGTGAAGGCTCGATCCCTGCCACCCGGGAG	477		
Db	325	ATGTTGGTCTAGAGGAATCCGGGGAGTGGTGAAGGCTCGATCCCTGCCACCCGGGAG	384		
Qy	478	GAGGGCTACATCCCAAGCAACTATGTGCGCCGCGTTGACTCTCTGGAGACAGAGGTGG	537		
Db	385	GAGGGCTACATCCCAAGCAACTATGTGCGCCGCGTTGACTCTCTGGAGACAGAGGTGG	444		
Qy	538	TTTTTCAAGGGCATCAGCCGGGAAGGACGAGAGCGCCAACTGCTGGCTCCCGGCAACATG	597		
Db	445	TTTTTCAAGGGCATCAGCCGGGAAGGACGAGAGCGCCAACTGCTGGCTCCCGGCAACATG	504		
Qy	598	CTGGGCTCTTCATGATCCGGGATACGAGACCCACTAAAGGAAGTACTCTTTGTCCTGG	657		
Db	505	CTGGGCTCTTCATGATCCGGGATACGAGACCCACTAAAGGAAGTACTCTTTGTCCTGG	564		
Qy	658	CGAGACTACGACCTCCGCGAGGAGATACCGTGAACATTTACAAGATCCGGACCTCGGAC	717		
Db	565	CGAGACTACGACCTCCGCGAGGAGATACCGTGAACATTTACAAGATCCGGACCTCGGAC	624		
Qy	718	AACGGGGCTTCTACATATATCCCGGAGACCTTTCAGCACTCTCAGAGAGTGTGGAC	777		
Db	625	AACGGGGCTTCTACATATATCCCGGAGACCTTTCAGCACTCTCAGAGAGTGTGGAC	684		
Qy	778	CACCTACAAGAGGGGAACGACGGCTCTGCCAGAACTCTGCTGCCCTGCTGCTGCTCC	837		
Db	685	CACCTACAAGAGGGGAACGACGGCTCTGCCAGAACTCTGCTGCCCTGCTGCTGCTCC	744		
Qy	838	AAGCCCCAGAGGCTTTGGGAGAAAGATGCTCTGGAGATCCCTCGGGAATCCCTCAAGCTG	897		
Db	745	AAGCCCCAGAGGCTTTGGGAGAAAGATGCTCTGGAGATCCCTCGGGAATCCCTCAAGCTG	804		
Qy	898	GAGAAAGAACTTGGAGCTGGGAGTGGGGAGTCTGGATGGCCACCTACAAACAGCAC	957		
Db	805	GAGAAAGAACTTGGAGCTGGGAGTGGGGAGTCTGGATGGCCACCTACAAACAGCAC	864		
Qy	958	ACCAAGTGGCAGTGAAGACAGTGAAGCCAGGAGCATGCTGCTGGAGGCTTCTCTGGCA	1017		
Db	865	ACCAAGTGGCAGTGAAGACAGTGAAGCCAGGAGCATGCTGCTGGAGGCTTCTCTGGCA	924		
Qy	1018	GAGGCCAAGCTGATGATAAACTCTGCAGCATGACAAGCTGGTCAAACTTCATCGGTGGTC	1077		
Db	925	GAGGCCAAGCTGATGATAAACTCTGCAGCATGACAAGCTGGTCAAACTTCATCGGTGGTC	984		
Qy	1078	ACCAAGGAGCCATCTACATCATCAGGAGTTCATGCGCCAAAGGAGCTTCTGACATTT	1137		
Db	985	ACCAAGGAGCCATCTACATCATCAGGAGTTCATGCGCCAAAGGAGCTTCTGACATTT	1044		
Qy	1138	CTGAAAAGTGATGAGGCGAGCAAGCCATTTGCCAAAATCTATTGACTTCTCAGCCAG	1197		
Db	1045	CTGAAAAGTGATGAGGCGAGCAAGCCATTTGCCAAAATCTATTGACTTCTCAGCCAG	1104		
Qy	1198	ATTGCAAGAGGCTGGCCTTTCATCGAGCAGAGAGGAACATACATCCACCGAGACCTCGAGCT	1257		

Db	1105	ATTTGCAAGAGGCATGGCTTCATCTGAGCAGAGAACTACATCCACGAGACCTCCGAGCT	1164
Qy	1258	GCCAAACATCTTGGTCTCTGTCATCCCTGGTGTTGAAGATTGCTGACTTTGGCTTGGCCCGG	1317
Db	1165	GCCAAACATCTTGGTCTCTGTCATCCCTGGTGTTGAAGATTGCTGACTTTGGCTTGGCCCGG	1224
Qy	1318	GTCAATTGAGACAACAGTAGTACACGGCTCGGGAAAGGGGCCAAGTTCGCCATCAAGTGGACA	1377
Db	1225	GTCAATTGAGACAACAGTAGTACACGGCTCGGGAAAGGGGCCAAGTTCGCCATCAAGTGGACA	1284
Qy	1378	GTCTCTGAAGCCATCAACTTTGGGCTCGTTACCATCAAGTCAAGCTCTGGTCTTTGGT	1437
Db	1285	GTCTCTGAAGCCATCAACTTTGGGCTCGTTACCATCAAGTCAAGTCAAGCTCTGGTCTTTGGT	1344
Qy	1438	ATCTCTGCTGATGAGATCGTCACTACGGCCGGATCCCTTACCCAGGAGTGTCAAAACCCCT	1497
Db	1345	ATCTCTGCTGATGAGATCGTCACTACGGCCGGATCCCTTACCCAGGAGTGTCAAAACCCCT	1404
Qy	1498	GAAGTGATCCGAGCTCTGGAGCGTGGATACCGGATGCCTCGCCACAGAAACTGCCACAG	1557
Db	1405	GAAGTGATCCGAGCTCTGGAGCGTGGATACCGGATGCCTCGCCACAGAAACTGCCACAG	1464
Qy	1558	GAGCTCTAACATCATGATCGCGTGTGGAATAAACCGTCCGAGGAGCGGCGACCTTC	1617
Db	1465	GAGCTCTAACATCATGATCGCGTGTGGAATAAACCGTCCGAGGAGCGGCGACCTTC	1524
Qy	1618	GAATACATCCAGAGTGTGCTGGATGACTTCTACACGGCCACACAGAGCCAGTACCAACAG	1677
Db	1525	GAATACATCCAGAGTGTGCTGGATGACTTCTACACGGCCACACAGAGCCAGTACCAACAG	1584
Qy	1678	CAGCCATGATAGGAGGAGCACGAGGCGAGGGGTGCCAGGTGGTGGCT	1729
Db	1585	CAGCCATGATAGGAGGAGCACGAGGCGAGGGGTGCCAGGTGGTGGCT	1636

RESULT 4	
ABL61214	
ID	ABL61214 standard; DNA; 183 BP.
XX	
AC	ABL61214;
XX	
DT	04-SEP-2002 (first entry)
XX	
DE	Human nucleotide fragment capable of inactivating HIV Nef protein.
XX	
KW	Nef protein; fusion protein; virucide; anti-HIV; accessory protein;
KW	pathogenicity; diagnosis; AIDS; human; ds.
XX	
OS	Homo sapiens.
XX	
PN	DE10109532-C1.
XX	
PD	13-JUN-2002.
XX	
PF	28-FEB-2001; 2001DE-1009532.
XX	
PR	28-FEB-2001; 2001DE-1009532.
XX	
PA	(GEYE/) GEYER M.
PA	(FACK/) FACKLER O.
XX	
PI	Geyer M;
XX	
DR	WPI; 2002-418264/45.
XX	
PT	New fusion protein that blocks Nef protein, useful for treatment or
PT	diagnosis of acquired immune deficiency syndrome, has high specificity
PT	and affinity -
XX	
PS	Claim 12; Page 14; 22pp; German.
XX	
CC	This invention describes a novel fusion protein for blocking the Nef

protein of human immune deficiency virus (HIV) which comprises: (i) protein domain 1 that binds to a di-leucine (LL) motif; (ii) a protein domain 2 that binds to a PxxP motif; and (iii) a polypeptide linker between protein domains 1 and 2. The products of the invention have virucide and anti-HIV activity and are capable of neutralising Nef, an accessory protein essential for pathogenicity of HIV-1. The fusion protein of the invention comprises the LL domain of the beta-subunit of the adapter-protein complex Ap-1 and the PxxP binding SH3 domain of tyrosine kinase Hck, linked through a 60 amino acid peptide. The products of the invention are used for *in vitro* diagnosis of AIDS and for treatment of AIDS. The LL and PxxP motifs are specific for Nef, which, unlike HIV protease, has no human homologue, so the fusion protein (which binds Nef with very high affinity) should cause essentially no side effects. This sequence represents a human derived nucleotide fragment used in the construction of the fusion protein of the invention and which contains a PXXP-motif binding motif useful to the invention.

Sequence 183 BP: 41 A; 50 C; 56 G; 36 T; 0 other;

	Query Match	9.1%;	Score 183;	DB 24;	Length 183;
	Best Local Similarity	100.0%;	Pred. No. 1.8e-79;		
	Matches 183;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	337	TCGTGAGGACATCATCGTGGTTCGCCCTGTATCATTTACGAGGCCATTACACGACGAAGACCTC	396		
Db					
	1	TCGTGAGGACATCATCGTGGTTCGCCCTGTATCATTTACGAGGCCATTACACGACGAAGACCTC	60		
Qy	397	AGCTTCCAGAAAGGGGACACAGATGGTGCTCTAGAGGAATCCGGGGAGTGGTGGGAAGGCT	456		
Db					
	61	AGCTTCCAGAAAGGGGACACAGATGGTGCTCTAGAGGAATCCGGGGAGTGGTGGGAAGGCT	120		
Qy	457	CGATCCCTGGCCACCCGGAAGGAGGGCTACATCCCAAGCAACTATGTGCGCCCGCGTTTGAC	516		
Db	121	CGATCCCTGGCCACCCGGAAGGAGGGCTACATCCCAAGCAACTATGTGCGCCCGCGTTTGAC	180		
Qy	517	TCT 519			
Db	181	TCT 183			

RESULT 5.	
ABL61215	
ID	ABL61215 standard; DNA; 1416 BP.
XX	
XX	ABL61215;
XX	
AC	
DT	04-SEP-2002 (first entry)
XX	
DE	Rat/human fusion construct capable of inactivating HIV Nef protein.
XX	
KW	Nef protein; fusion protein; virucide; anti-HIV; accessory protein;
KW	pathogenicity; diagnosis; AIDS; rat; human; ds.
XX	
XX	Rattus sp.
OS	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	DE10109532-C1.
PN	
XX	13-JUN-2002.
PD	
XX	
XX	28-FEB-2001; 2001DE-1009532.
PF	
XX	
XX	28-FEB-2001; 2001DE-1009532.
PR	
XX	
XX	(GEYE/) GEYER M.
PA	(FACK/) FACKLER O.
XX	
XX	Geyer M;
PI	
XX	WPI; 2002-418264/45.
DR	
XX	
XX	New fusion protein that blocks Nef protein, useful for treatment or

PT diagnosis of acquired immune deficiency syndrome, has high specificity
 XX and affinity
 PS Claim 13; Page 14-15; 22pp; German.
 XX
 CC This invention describes a novel fusion protein for blocking the Nef
 CC protein of human immune deficiency virus (HIV) which comprises: (i)
 CC protein domain 1 that binds to a di-leucine (LL) motif; (ii) a
 CC protein domain 2 that binds to a Pxxp motif; and (iii) a polypeptide
 CC linker between protein domains 1 and 2. The products of the invention
 CC have virucide and anti-HIV activity and are capable of neutralising Nef,
 CC an accessory protein essential for pathogenicity of HIV-1. The fusion
 CC protein of the invention comprises the LL domain of the beta-subunit of
 CC tyrosine kinase Hck, linked through a 60 amino acid peptide. The products
 CC of the invention are used for in vitro diagnosis of AIDS and for
 CC treatment of AIDS. The LL and Pxxp motifs are specific for Nef, which,
 CC unlike HIV protease, has no human homologue, so the fusion protein (which
 CC binds Nef with very high affinity) should cause essentially no side
 CC effects. This sequence represents a fusion construct composed of a rat
 CC nucleotide fragment which contains a dileucine (LL) motif and a human
 CC nucleotide fragment containing a Pxxp-motif binding domain useful to the
 CC invention.
 XX
 SQ Sequence 1416 BP; 340 A; 383 C; 386 G; 307 T; 0 other;
 Query Match 9.0%; Score 181; DB 24; Length 1416;
 Best Local Similarity 100.0%; Pred. No. 1.8e-78;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 339 TGAGGACATCATCGTGGTTCCTGTATGATTACGAGGCCATTCACCACGAAGACCTCAG 398
 DB 1233 TGAGGACATCATCGTGGTTCCTGTATGATTACGAGGCCATTCACCACGAAGACCTCAG 1292
 QY 399 CTTCCAGAGGGGACACAGATGGTCTTAGAGGAATCCGGGAGTGGTGAAGGCTCG 458
 DB 1293 CTTCCAGAGGGGACACAGATGGTGGTCTTAGAGGAATCCGGGAGTGGTGAAGGCTCG 1352
 QY 459 ATCCCTGGCCACCCGGAAGGAGGCTACATCCCAAGCAACTATGTCCCGCGTTGACTC 518
 DB 1353 ATCCCTGGCCACCCGGAAGGAGGCTACATCCCAAGCAACTATGTCCCGCGTTGACTC 1412
 QY 519 T 519
 DB 1413 T 1413
 RESULT 6
 ABL61216
 ID ABL61216 standard; DNA; 1542 BP.
 XX
 AC ABL61216;
 XX
 DT 04-SEP-2002 (first entry)
 XX
 DE Rat/human fusion construct capable of inactivating HIV Nef protein.
 XX
 KW Nef protein; fusion protein; virucide; anti-HIV; accessory protein;
 KW pathogenicity; diagnosis; AIDS; rat; human; ds.
 XX
 OS Rattus sp.
 OS Homo sapiens.
 OS Synthetic.
 PN DE10109532-C1.
 XX
 XX 13-JUN-2002.
 PD
 XX 28-FEB-2001; 2001DE-1009532.
 PF
 XX 28-FEB-2001; 2001DE-1009532.
 PR
 XX (GEYE/) GEYER M.

PA (PACK/) FACKLER O.
 XX
 PI Geyer M;
 XX
 DR WPI; 2002-418264/45.
 XX
 PT New fusion protein that blocks Nef protein, useful for treatment or
 PT diagnosis of acquired immune deficiency syndrome, has high specificity
 PT and affinity
 XX
 PS Claim 16; Page 15-16; 22pp; German.
 XX
 CC This invention describes a novel fusion protein for blocking the Nef
 CC protein of human immune deficiency virus (HIV) which comprises: (i)
 CC protein domain 1 that binds to a di-leucine (LL) motif; (ii) a
 CC protein domain 2 that binds to a Pxxp motif; and (iii) a polypeptide
 CC linker between protein domains 1 and 2. The products of the invention
 CC have virucide and anti-HIV activity and are capable of neutralising Nef,
 CC an accessory protein essential for pathogenicity of HIV-1. The fusion
 CC protein of the invention comprises the LL domain of the beta-subunit of
 CC the adapter-protein complex AP-1 and the Pxxp binding SH3 domain of
 CC tyrosine kinase Hck, linked through a 60 amino acid peptide. The products
 CC of the invention are used for in vitro diagnosis of AIDS and for
 CC treatment of AIDS. The LL and Pxxp motifs are specific for Nef, which,
 CC unlike HIV protease, has no human homologue, so the fusion protein (which
 CC binds Nef with very high affinity) should cause essentially no side
 CC effects. This sequence represents a fusion construct composed of a rat
 CC nucleotide fragment which contains a dileucine (LL) motif and a human
 CC nucleotide fragment containing a Pxxp-motif binding domain useful to the
 CC invention.
 XX
 SQ Sequence 1542 BP; 369 A; 419 C; 427 G; 327 T; 0 other;
 Query Match 9.0%; Score 181; DB 24; Length 1542;
 Best Local Similarity 100.0%; Pred. No. 1.8e-78;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 339 TGAGGACATCATCGTGGTTCCTGTATGATTACGAGGCCATTCACCACGAAGACCTCAG 398
 DB 1290 TGAGGACATCATCGTGGTTCCTGTATGATTACGAGGCCATTCACCACGAAGACCTCAG 1349
 QY 399 CTTCCAGAGGGGACACAGATGGTCTTAGAGGAATCCGGGAGTGGTGAAGGCTCG 458
 DB 1350 CTTCCAGAGGGGACACAGATGGTCTTAGAGGAATCCGGGAGTGGTGAAGGCTCG 1409
 QY 459 ATCCCTGGCCACCCGGAAGGAGGCTACATCCCAAGCAACTATGTCCCGCGTTGACTC 518
 DB 1410 ATCCCTGGCCACCCGGAAGGAGGCTACATCCCAAGCAACTATGTCCCGCGTTGACTC 1469
 QY 519 T 519
 DB 1470 T 1470
 RESULT 7
 AAT19957
 ID AAT19957 standard; CDNA to mRNA; 369 BP.
 XX
 AC AAT19957;
 XX
 DT 17-JUL-1996 (first entry)
 XX
 DE Human gene signature HUMGS01089.
 XX
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9514772-A1.
 PN
 XX 01-JUN-1995.

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XX 11-NOV-1994; 94WO-JP01916.
PF 12-NOV-1993; 93JP-0355504.
XX (MATSU) MATSUBARA K.
PA (OKUBO) OKUBO K.
XX Matsubara K, Okubo K;
PI WPI; 1995-206931/27.
DR WPI; 1995-206931/27.
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
PS Claim 1; Page 520; 2245pp; Japanese.
XX A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridize to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridize with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
SQ Sequence 369 BP; 82 A; 97 C; 102 G; 75 T; 13 other;

Query Match 8.4%; Score 169; DB 16; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.4e-72;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1535 CTCGCCAGAGAACTGCCAGAGAGCTCTACAAATCATGATGCGCTCGGAAACCC 1594
DB 33 CTCGCCAGAGAACTGCCAGAGAGCTCTACAAATCATGATGCGCTCGGAAACCC 92
QY 1595 GTCGGGAGGAGCGCGACCTTCGAATACATCCAGAGTGTGCTGGATGACTTCTACACGG 1654
DB 93 GTCGGGAGGAGCGCGACCTTCGAATACATCCAGAGTGTGCTGGATGACTTCTACACGG 152
QY 1655 CCACAGAGCCAGTACCAACACAGCAGCCATGATAGGAGGACCGGCA 1703
DB 153 CCACAGAGCCAGTACCAACACAGCAGCCATGATAGGAGGACCGGCA 201

RESULT 8
ABA50558
ID ABA50558 standard; DNA; 171 BP.
XX ABA50558;
XX
XX 01-FEB-2002 (first entry)
XX Human breast cell single exon nucleic acid probe #9253.
DE Human breast cell single exon nucleic acid probe #9253.
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO200157271-A2.
PN WO200157271-A2.
XX 09-AUG-2001.
PD 09-AUG-2001.
XX
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PF 30-JAN-2001; 2001WO-US000662.
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX Claim 4; SEQ ID NO 9253; 327pp + sequence listing; English.
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and Br 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGGCCAACTTCCCATCAAGTGGACAGCTCTGAAGCCATCAACTTTGGCTCTTCACCA 1411
DB 1 GGGCCAACTTCCCATCAAGTGGACAGCTCTGAAGCCATCAACTTTGGCTCTTCACCA 60
QY 1412 TCAAGTCAGACGTCTGGTCTTTGGTATCTCTGATGGAGATCGTCACCTACGGCGGA 1471
DB 61 TCAAGTCAGACGTCTGGTCTTTGGTATCTCTGATGGAGATCGTCACCTACGGCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133

RESULT 9
ABA68516
ID ABA68516 standard; DNA; 171 BP.
XX ABA68516;
XX 01-FEB-2002 (first entry)
XX Human foetal liver single exon nucleic acid probe #16821.
DE Human foetal liver single exon nucleic acid probe #16821.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
OS Homo sapiens.
```

```
XX WO200157277-A2.
PN
XX
XX
PD
XX
XX
PF
XX
XX
XX
30-JAN-2001; 2001WO-US00669.
XX
XX
XX
04-FEB-2000; 2000US-0180312.
PR
XX
XX
26-MAY-2000; 2000US-0207456.
PR
XX
XX
30-JUN-2000; 2000US-0608408.
PR
XX
XX
03-AUG-2000; 2000US-0632366.
PR
XX
XX
21-SEP-2000; 2000US-0234687.
PR
XX
XX
27-SEP-2000; 2000US-0236359.
PR
XX
XX
04-OCT-2000; 2000GB-0024263.
XX
XX
PA
(MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI
Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
WPI; 2001-483447/52.
XX
XX
DR
Human genome-derived single exon nucleic acid probes useful for
PT
analyzing gene expression in human fetal liver -
XX
XX
PS
Claim 4; SEQ ID NO 16821; 639pp + sequence listing; English.
XX
XX
CC
The invention relates to a single exon nucleic acid probe for
CC
measuring human gene expression in a sample derived from human foetal
CC
liver. The single exon nucleic acid probes may be used for predicting,
CC
measuring and displaying gene expression in samples derived from human
CC
fetal liver. The present sequence is a single exon nucleic acid
CC
probe of the invention.
CC
Note: The sequence data for this patent did not form part of the
CC
printed specification, but was obtained in electronic format directly
CC
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ
Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGGCCAAGTTCCTCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 1471
Db 1 GGGCCAAGTTCCTCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 60

QY 1412 TCAAGTCAGACGTCCTGCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 1471
Db 61 TCAAGTCAGACGTCCTGCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 120

QY 1472 TCCCTTACCCAGG 1484
Db 121 TCCCTTACCCAGG 133

RESULT 10
ABA35497
ID ABA35497 standard; DNA; 171 BP.
XX
XX
AC ABA35497;
XX
XX
DT 23-JAN-2002 (first entry)
XX
XX
DE Probe #13963 for gene expression analysis in human heart cell sample.
XX
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157274-A2.
XX
```

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PD
XX
XX
XX
30-JAN-2001; 2001WO-US00666.
XX
XX
XX
04-FEB-2000; 2000US-0180312.
PR
XX
XX
26-MAY-2000; 2000US-0207456.
PR
XX
XX
30-JUN-2000; 2000US-0608408.
PR
XX
XX
03-AUG-2000; 2000US-0632366.
PR
XX
XX
21-SEP-2000; 2000US-0234687.
PR
XX
XX
27-SEP-2000; 2000US-0236359.
PR
XX
XX
04-OCT-2000; 2000GB-0024263.
XX
XX
PA
(MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI
Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
WPI; 2001-488899/53.
XX
XX
DR
Single exon nucleic acid probes for analyzing gene expression in human
PT
hearts -
XX
XX
PS
Claim 4; SEQ ID NO 13963; 530pp; English.
XX
XX
CC
The present invention relates to single exon nucleic acid probes for
CC
measuring human gene expression in a sample derived from human heart. The
CC
present sequence is one such probe. The probes may be used for
CC
predicting, measuring and displaying gene expression in samples derived
CC
from the human heart via microarrays. By measuring gene expression, the
CC
probes are useful for predicting, diagnosing, grading, staging,
CC
monitoring and prognosing diseases of the human heart and vascular system
CC
e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC
congenital heart disease.
CC
Note: The sequence data for this patent did not form part of the printed
CC
specification, but was obtained in electronic format directly from WIPO
CC
at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ
Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGGCCAAGTTCCTCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 1471
Db 1 GGGCCAAGTTCCTCCATCAAGTGGACAGCTCCTGATGAGATCGTCACCTACGCCGGA 60

QY 1412 TCAAGTCAGACGTCCTGCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 1471
Db 61 TCAAGTCAGACGTCCTGCTTGGTATCCTGCTGATGAGATCGTCACCTACGCCGGA 120

QY 1472 TCCCTTACCCAGG 1484
Db 121 TCCCTTACCCAGG 133

RESULT 11
AAK16884
ID AAK16884 standard; DNA; 171 BP.
XX
XX
AC AAK16884;
XX
XX
DT 05-NOV-2001 (first entry)
XX
XX
DE Human brain expressed single exon probe SEQ ID NO: 16875.
XX
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157275-A2.
XX
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PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
PT
XX Example 4; SEQ ID NO: 16875; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
XX - Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
SQ
Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1352 GGGCCAAGTTCCCATCAAGTGGACAGCTCTCTGAAGCCATCAACTTTGGCTCCTTCACCA 1411
DB 1 GGGCCAAGTTCCCATCAAGTGGACAGCTCTCTGAAGCCATCAACTTTGGCTCCTTCACCA 60
QY 1412 TCAAGTCAGACGCTGTGGTCTCTTGGTATCCTGATGAGATCGTCACCTACGCGCGGA 1471
DB 61 TCAAGTCAGACGCTGTGGTCTCTTGGTATCCTGATGAGATCGTCACCTACGCGCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133
RESULT 12
AAK42654
ID AAK42654 standard; DNA; 171 BP.
XX
AC AAK42654;
XX
XX 06-NOV-2001 (first entry)
DT
XX Human bone marrow expressed single exon probe SEQ ID NO: 17211.
DE
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
OS
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
PT
XX Example 4; SEQ ID NO: 16875; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
XX - Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
SQ
Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1352 GGGCCAAGTTCCCATCAAGTGGACAGCTCTCTGAAGCCATCAACTTTGGCTCCTTCACCA 1411
DB 1 GGGCCAAGTTCCCATCAAGTGGACAGCTCTCTGAAGCCATCAACTTTGGCTCCTTCACCA 60
QY 1412 TCAAGTCAGACGCTGTGGTCTCTTGGTATCCTGATGAGATCGTCACCTACGCGCGGA 1471
DB 61 TCAAGTCAGACGCTGTGGTCTCTTGGTATCCTGATGAGATCGTCACCTACGCGCGGA 120
QY 1472 TCCCTTACCCAGG 1484
DB 121 TCCCTTACCCAGG 133
RESULT 13
AAI23408
ID AAI23408 standard; DNA; 171 BP.
XX
AC AAI23408;
XX
XX 12-OCT-2001 (first entry)
DT
XX Probe #13341 for gene expression analysis in human cervical cell sample.
DE
XX Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
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XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX Claim 25; SEQ ID No 13341; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
SQ

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGCCCAAGTCCCATCAAGTGGAGAGCTCTGAGCCATCAACTTTGGCTCCTTCACCA 1411
DB 1 GGCCCAAGTCCCATCAAGTGGAGAGCTCTGAGCCATCAACTTTGGCTCCTTCACCA 60

QY 1412 TCAAGTCAGAGCTCTGGTTCCTGCTGATGGAGATCGTCACCTACGCCGGA 1471
DB 61 TCAAGTCAGAGCTCTGGTTCCTGCTGATGGAGATCGTCACCTACGCCGGA 120

QY 1472 TCCCTTACCAGG 1484
DB 121 TCCCTTACCAGG 133

RESULT 14
AAI48728
ID AAI48728 standard; DNA; 171 BP.
AC AAI48728;
XX 17-OCT-2001 (first entry)
XX Probe #17414 used to measure gene expression in human placenta sample.
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00663.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI; 2001-48897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 25; SEQ ID No 17414; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;
SQ

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGCCCAAGTCCCATCAAGTGGAGAGCTCTGAGCCATCAACTTTGGCTCCTTCACCA 1411
DB 1 GGCCCAAGTCCCATCAAGTGGAGAGCTCTGAGCCATCAACTTTGGCTCCTTCACCA 60

QY 1412 TCAAGTCAGAGCTCTGGTTCCTGCTGATGGAGATCGTCACCTACGCCGGA 1471
DB 61 TCAAGTCAGAGCTCTGGTTCCTGCTGATGGAGATCGTCACCTACGCCGGA 120

QY 1472 TCCCTTACCAGG 1484
DB 121 TCCCTTACCAGG 133

RESULT 15
AAI09035
ID AAI09035 standard; DNA; 171 BP.
AC AAI09035;
XX 09-OCT-2001 (first entry)
XX Probe #9026 used to measure gene expression in human breast sample.
XX Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX Homo sapiens.
XX WO200157270-A2.
XX 09-AUG-2001.
XX 29-JAN-2001; 2001WO-US00661.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX Claim 25; SEQ ID No 9026; 322pp; English.
XX The present invention relates to novel single exon nucleic acid probes.
XX

CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 171 BP; 35 A; 53 C; 46 G; 37 T; 0 other;

Query Match 6.6%; Score 133; DB 22; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.1e-55;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1352 GGGCCAAGTTCCCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCCTTCACCA 1411
Db 1 GGGCCAAGTTCCCCCATCAAGTGGACAGCTCCTGAAGCCATCAACTTTGGCTCCTTCACCA 60
Qy 1412 TCAAGTCAGAGCTGTGCTTGGTATCCTGCTGATGGAGATCGTCACCTACGCCGGA 1471
Db 61 TCAAGTCAGAGCTGTGCTTGGTATCCTGCTGATGGAGATCGTCACCTACGCCGGA 120
Qy 1472 TCCCTTACCCAGG 1484
Db 121 TCCCTTACCCAGG 133

Search completed: July 4, 2003, 02:31:01
Job time : 458 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2003, 04:47:18 ; Search time 458 Seconds
(without alignments)
9907.809 Million cell updates/sec

Title: US-10-007-010-3

Perfect score: 2015

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	1.5	31	AAI30734	Human single nucle
2	31	1.5	31	AAI30735	Human single nucle
3	31	1.5	31	AAI30736	Human single nucle
4	31	1.5	31	AAI30737	Human single nucle
5	31	1.5	31	AAI30738	Human single nucle
6	27	1.3	33	AAH41498	Human tyrosine kin
7	26	1.3	32	AAH41491	Human tyrosine kin
8	26	1.3	32	AAH41492	Human tyrosine kin
9	25	1.2	32	AAH41501	Human tyrosine kin

10	25	1.2	51	23	ABL00375	Human silent nonco
11	24	1.2	32	22	AAH41500	Human tyrosine kin
12	24	1.2	78	22	AAC90044	PCR primer used to
13	21	1.0	21	22	AAF95624	Human gene single
14	21	1.0	21	22	AAF95625	Human gene single
15	21	1.0	21	22	AAF95626	Human gene single
16	21	1.0	21	22	AAF95627	Human gene single
17	21	1.0	21	22	AAF95628	Human gene single
18	21	1.0	21	22	AAF95629	Human gene single
19	21	1.0	21	22	AAF95630	Human gene single
20	20	1.0	21	16	AAT41207	Human gene signatu
21	20	1.0	21	16	AAT41208	Human gene signatu
22	19	0.9	51	22	AAI33024	Human SNP oligonuc
23	19	0.9	51	22	AAI33025	Human SNP oligonuc
24	18	0.9	19	21	AAH82879	cdk4 ribozyme bind
25	18	0.9	19	22	AAH58041	Cell-cycle depende
26	18	0.9	20	20	AAH29342	Chemically modifie
27	18	0.9	20	20	AAH29331	JNK2-specific prob
28	18	0.9	20	21	AAC62874	JNK antisense olig
29	18	0.9	20	21	AAC62885	JNK antisense olig
30	18	0.9	20	21	AAA48651	Antisense oligonuc
31	18	0.9	20	22	AAH23754	JNK1 antisense oli
32	18	0.9	20	22	AAF99183	Immunostimulatory
33	18	0.9	20	24	ABL39057	Immunostimulatory
34	18	0.9	34	22	AAH41497	Human tyrosine kin
35	18	0.9	48	24	ABK30196	CYP2D6 gene polymo
36	18	0.9	51	24	ABK30195	CYP2D6 gene polymo
37	17	0.8	19	21	AAH82878	cdk4 ribozyme bind
38	17	0.8	19	22	AAH58040	Cell-cycle depende
39	17	0.8	20	20	AAH01356	PCR primer for mou
40	17	0.8	20	22	AAF72970	Human daxx inhibit
41	17	0.8	21	24	ABK40441	Forward PCR primer
42	17	0.8	23	14	AAQ43744	prk primer prk2.
43	17	0.8	23	16	AAT03086	Protein tyrosine-k
44	17	0.8	25	21	AAZ37264	PCR primer for SGR
45	17	0.8	57	22	AAH04769	Synthetic gene shG

ALIGNMENTS

RESULT 1

AAI30734

ID AAI30734 standard; DNA; 31 BP.

XX AAI30734;

AC AAI30734;

XX 18-OCT-2001 (first entry)

DT 18-OCT-2001 (first entry)

XX Human single nucleotide polymorphism (SNP) HCK 1.

DE Human; ressequenc; genotype; disease; forensic; paternity testing;

XX single nucleotide polymorphism; SNP; ss.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

FT Variation

FT replace(16,T)

FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

PN WO200156800-A2.

XX 13-SEP-2001.

PD 07-MAR-2001; 2001WO-US07268.

XX 07-MAR-2000; 2000US-0187510.

XX 22-MAY-2000; 2000US-0206129.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

PI


```
SQ Sequence 31 BP; 6 A; 9 C; 6 G; 10 T; 0 other;
Query Match 1.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1405 TTCACATCAAGTCAGACGTCGTGGTCCCTTTG 1435
Db 1 TTCACATCAAGTCAGACGTCGTGGTCCCTTTG 31

RESULT 4
AAI30737
ID AAI30737 standard; DNA; 31 BP.
XX
AC AAI30737;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) HCK 4.
XX
KW Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(16,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
WPI; 2001-522952/57.
XX
Nucleic acid molecules from the human genome which include polymorphic
sites, useful in methods for predicting the presence, absence or
severity of a particular phenotype or disorder (e.g. diabetes)
associated with a particular genotype -
XX
Claim 1; Page 104; 145pp; English.
XX
The invention relates to the identification of nucleic acid molecules
(AAI29513-AAI31314) from the human genome which include polymorphic sites
of individuals were resequenced and single nucleotide polymorphisms
(SNPs) in these genes discovered. The method is useful for predicting the
presence, absence or severity of a particular phenotype or disorder (e.g.
diabetes) associated with a particular genotype. The nucleic acids
containing the polymorphic sites may be useful in forensics and paternity
testing.
XX
Sequence 31 BP; 7 A; 7 C; 10 G; 7 T; 0 other;
Query Match 1.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 GTTGGGGAAGTCGTGGATGGCCACCTACAC 951
Db 1 GTTGGGGAAGTCGTGGATGGCCACCTACAC 31

RESULT 5
AAI30738
ID AAI30738 standard; DNA; 31 BP.
XX
AC AAI30738;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) HCK 5.
XX
KW Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(16,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
WPI; 2001-522952/57.
XX
Nucleic acid molecules from the human genome which include polymorphic
sites, useful in methods for predicting the presence, absence or
severity of a particular phenotype or disorder (e.g. diabetes)
associated with a particular genotype -
XX
Claim 1; Page 104; 145pp; English.
XX
The invention relates to the identification of nucleic acid molecules
(AAI29513-AAI31314) from the human genome which include polymorphic sites
of individuals were resequenced and single nucleotide polymorphisms
(SNPs) in these genes discovered. The method is useful for predicting the
presence, absence or severity of a particular phenotype or disorder (e.g.
diabetes) associated with a particular genotype. The nucleic acids
containing the polymorphic sites may be useful in forensics and paternity
testing.
XX
Sequence 31 BP; 12 A; 11 C; 5 G; 3 T; 0 other;
Query Match 1.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 AAAAAGTGAACAGCCAGCCAGCCACACTGT 249
Db 1 AAAAAGTGAACAGCCAGCCAGCCACACTGT 31

RESULT 6
AAH41498/c
ID AAH41498 standard; DNA; 33 BP.
XX
AC AAH41498;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human tyrosine kinase Hck PCR primer SEQ ID NO:10.
```

```
XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
XX KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
XX KW Hck signal transduction; human immunodeficiency virus; HIV infection;
XX KW anticancer; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200132869-A1.
XX PD 10-MAY-2001.
XX PF 26-OCT-2000; 2000WO-JP07500.
XX PR 29-OCT-1999; 99JP-0309957.
XX PS (SSSE ) SSP CO LTD.
XX PA Taniyama T, Narita T;
XX PI WPI; 2001-316440/33.
XX DR New proteins which bind to human tyrosine kinase Hck for promotion of
XX PT apoptosis and for the elucidation of the mechanism of Hck signal
XX PT transduction
XX XX
XX PS Example 3; Page 33; 45pp; Japanese.
XX CC The present invention describes a protein, designated HSB-1, which binds
XX CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
XX CC encoding the protein and its derivatives; (2) recombinant vectors
XX CC containing the nucleic acids; and (3) host cells transformed by the
XX CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
XX CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
XX CC of Hck signal transduction and of the role of Hck in human
XX CC immunodeficiency virus (HIV) infection. They can be used for the
XX CC treatment of infections and other diseases with which Hck is associated.
XX CC They promote the anticancer activity of tumour necrosis factor alpha.
XX CC The present sequence represents a PCR primer for the human tyrosine
XX CC kinase Hck, which is used in an example from the present invention.
XX SQ Sequence 33 BP; 2 A; 8 C; 11 G; 12 T; 0 other;

Query Match 1.3%; Score 27; DB 22; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1657 ACAGAGAGCCAGTACCAACAGCAGCCCA 1683
Db 33 ACAGAGAGCCAGTACCAACAGCAGCCCA 7

RESULT 7
AAH41491
ID AAH41491 standard; DNA; 32 BP.
XX AC AAH41491;
XX XX
XX DT 23-AUG-2001 (first entry)
XX DE Human tyrosine kinase Hck binding protein cloning PCR primer SEQ.3.
XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
XX KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
XX KW Hck signal transduction; human immunodeficiency virus; HIV infection;
XX KW anticancer; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200132869-A1.
XX PD 10-MAY-2001.
```

```
XX PF 26-OCT-2000; 2000WO-JP07500.
XX PR 29-OCT-1999; 99JP-0309957.
XX PA (SSSE ) SSP CO LTD.
XX PI Taniyama T, Narita T;
XX DR WPI; 2001-316440/33.
XX PT New proteins which bind to human tyrosine kinase Hck for promotion of
XX PT apoptosis and for the elucidation of the mechanism of Hck signal
XX PT transduction
XX XX
XX PS Example 1; Page 30; 45pp; Japanese.
XX CC The present invention describes a protein, designated HSB-1, which binds
XX CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
XX CC encoding the protein and its derivatives; (2) recombinant vectors
XX CC containing the nucleic acids; and (3) host cells transformed by the
XX CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
XX CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
XX CC of Hck signal transduction and of the role of Hck in human
XX CC immunodeficiency virus (HIV) infection. They can be used for the
XX CC treatment of infections and other diseases with which Hck is associated.
XX CC They promote the anticancer activity of tumour necrosis factor alpha.
XX CC The present sequence represents a PCR primer used in the cloning of
XX CC HSB-1, which is used in an example from the present invention.
XX SQ Sequence 32 BP; 8 A; 5 C; 9 G; 10 T; 0 other;

Query Match 1.3%; Score 26; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 TCGTGGTTGCCCTGTATGATTACGAG 375
Db 7 TCGTGGTTGCCCTGTATGATTACGAG 32

RESULT 8
AAH41492/c
ID AAH41492 standard; DNA; 32 BP.
XX AC AAH41492;
XX XX
XX DT 23-AUG-2001 (first entry)
XX DE Human tyrosine kinase Hck binding protein cloning PCR primer SEQ.4.
XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
XX KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
XX KW Hck signal transduction; human immunodeficiency virus; HIV infection;
XX KW anticancer; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200132869-A1.
XX PD 10-MAY-2001.
XX PF 26-OCT-2000; 2000WO-JP07500.
XX PR 29-OCT-1999; 99JP-0309957.
XX PA (SSSE ) SSP CO LTD.
XX PI Taniyama T, Narita T;
XX DR WPI; 2001-316440/33.
XX PD
```

PT New proteins which bind to human tyrosine kinase Hck for promotion of
PT apoptosis and for the elucidation of the mechanism of Hck signal
PT transduction -
XX
PS
PS Example 1; Page 31; 45pp; Japanese.
XX
CC The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transformed by the
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha.
CC The present sequence represents a PCR primer used in the cloning of
CC HSB-1, which is used in an example from the present invention.
XX
XX Sequence 32 BP; 7 A; 10 C; 9 G; 6 T; 0 other;
SQ
Query Match 1.3%; Score 26; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 796 GACGGGCTCTGCCAGAACTGTCGGT 821
DB 32 GACGGGCTCTGCCAGAACTGTCGGT 7
RESULT 9
AAH41501/C
ID AAH41501 standard; DNA; 32 BP.
XX
AC AAH41501;
XX
XX 23-AUG-2001 (first entry)
DT
XX Human tyrosine kinase Hck binding protein cloning PCR primer SEQ:15.
DE
XX Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200132869-A1.
PN
XX 10-MAY-2001.
PD
XX 26-OCT-2000; 2000WO-JP07500.
PF
XX 29-OCT-1999; 99JP-0309957.
PR
XX (SSSE) SSP CO LTD.
PA
XX Taniyama T, Narita T;
PI
XX WPI; 2001-316440/33.
DR
XX
XX New proteins which bind to human tyrosine kinase Hck for promotion of
PT apoptosis and for the elucidation of the mechanism of Hck signal
PT transduction -
XX
XX Example 4; Page 41; 45pp; Japanese.
PS
XX The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transformed by the
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds

CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha.
CC The present sequence represents a PCR primer used in the cloning of
CC HSB-1, which is used in an example from the present invention.
XX
XX Sequence 32 BP; 8 A; 9 C; 10 G; 5 T; 0 other;
SQ
Query Match 1.2%; Score 25; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 505 GCCCGCGTGTGACTCTCTCGAGACAG 529
DB 32 GCCCGCGTGTGACTCTCTCGAGACAG 8
RESULT 10
ABL00375
ID ABL00375 standard; DNA; 51 BP.
XX
AC ABL00375;
XX
DT 05-MAR-2002 (first entry)
DT
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:366.
DE
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX
XX Homo sapiens.
OS
XX WO200138586-A2.
PN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-US32311.
PF
XX 24-NOV-1999; 99US-0167383.
PR
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-355949/37.
DR
XX Isolated human nucleic acids comprising one or more single nucleotide
XX polymorphisms, useful for treating a subject suffering from a
XX pathology, e.g. autoimmune diseases, ascribed to the presence of a
XX sequence polymorphism -
XX
XX Claim 1; Page 359; 674pp; English.
PS
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the

CC polymorphic protein within appropriate physiological samples).

XX
SQ Sequence 51 BP; 10 A; 17 C; 13 G; 11 T; 0 other;
Query Match 1.2%; Score 25; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 GGGGCTTCTACATATCCCGCGAAG 746
|||||
Db 1 GGGGCTTCTACATATCCCGCGAAG 25

RESULT 11

AAH41500
ID AAH41500 standard; DNA; 32 BP.

XX
AC AAH41500;

XX
DT 23-AUG-2001 (first entry)

XX Human tyrosine kinase Hck binding protein cloning PCR primer SEQ:14.

XX Human; tyrosine kinase Hck binding protein; tyrosine kinase: Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer; PCR primer; ss.

XX OS Homo sapiens.

XX WO200132869-A1.

XX
PD 10-MAY-2001.

XX PF 26-OCT-2000; 2000WO-JP07500.

XX PR 29-OCT-1999; 99JP-0309957.

XX (SSSE) SSP CO LTD.

XX Taniyama T, Narita T;

XX WPI; 2001-316440/33.

XX New proteins which bind to human tyrosine kinase Hck for promotion of
PT apoptosis and for the elucidation of the mechanism of Hck signal
PT transduction

XX Example 4; Page 41; 45pp; Japanese.

XX The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transfected by the
CC vectors and expressing the protein. HSB-1 has cytosolic activity, binds
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha.
CC The present sequence represents a PCR primer used in the cloning of
CC HSB-1, which is used in an example from the present invention.

XX Sequence .32 BP; 9 A; 4 C; 10 G; 9 T; 0 other;

XX Query Match 1.2%; Score 24; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 GAGGAGTGGTTTTCAGGGCATC 552
|||||

Db 9 GAGGAGTGGTTTTCAGGGCATC 32

RESULT 12

AAC90044

ID AAC90044 standard; DNA; 78 BP.

XX
AC AAC90044;

XX 13-MAR-2001 (first entry)

XX PCR primer used to create a library of RRT-Hck SH3 domains.

XX SH3 domain; human; Src homology region 3 domain; RT-loop; Hck protein;
KW PCR primer; ss.

XX OS Homo sapiens.

XX WO200072742-A2.

XX PD 07-DEC-2000.

XX 26-MAY-2000; 2000WO-FI00477.

XX 26-MAY-1999; 99US-0136085.

XX (SAKS/) SAKSELA K.

XX Saksela K, Hiipakka M;

XX WPI; 2001-061424/07.

XX A method for generating Src homology region 3 (SH3) domains with
PT tailored binding properties or artificial SH3 domains, comprises
PT employing random manipulation of the SH3 RT-loop sequence

XX Example 1; Page 10; 34pp; English.

XX The present invention relates to a method for generating Src homology
CC region 3 (SH3) domains with tailored binding properties. The method
CC comprises producing a collection of SH3 domains containing a randomised
CC RT-loop (RRT-SH3 domains). Human p59 Hck was used in the present
CC invention as the SH3 domain. The present sequence is a PCR primer, which
CC was used to create a library of RRT-Hck SH3 domains. The generated SH3
CC domains are useful for inhibiting, activating or modifying the functions
CC of cellular or pathogen-encoded proteins for research or therapeutic
CC purposes.

XX SQ Sequence 78 BP; 13 A; 13 C; 17 G; 17 T; 18 other;

XX Query Match 1.2%; Score 24; DB 22; Length 78;

XX Best Local Similarity 100.0%; Pred. No. 0.28;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GACCTCAGCTTCCAGAGGGGAC 414
|||||

Db 55 GACCTCAGCTTCCAGAGGGGAC 78

RESULT 13

AAF95624

ID AAF95624 standard; DNA; 21 BP.

XX
AC AAF95624;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #385.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.

```
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US24503.
XX
XX 10-SEP-1999; 99US-0153357.
XX 26-JUL-2000; 2000US-0220947.
XX 16-AUG-2000; 2000US-0225724.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis -
XX
XX Examples; Page 75; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism
XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification.
XX
XX Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 CCGCGTTGACCTCTCTGGAGAC 527
Db 1 CCGCGTTGACCTCTCTGGAGAC 21

RESULT 14
AAF95625
ID AAF95625 standard; DNA; 21 BP.
XX
XX AAF95625;
XX
XX 06-JUN-2001 (first entry)
XX
XX Human gene single nucleotide polymorphism #386.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(11,T)
```

```
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US24503.
XX
XX 10-SEP-1999; 99US-0153357.
XX 26-JUL-2000; 2000US-0220947.
XX 16-AUG-2000; 2000US-0225724.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis -
XX
XX Examples; Page 75; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism
XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification.
XX
XX Sequence 21 BP; 8 A; 4 C; 7 G; 2 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 773 TGGACCACCTACAGAGGGGA 793
Db 1 TGGACCACCTACAGAGGGGA 21

RESULT 15
AAF95626
ID AAF95626 standard; DNA; 21 BP.
XX
XX AAF95626;
XX
XX 06-JUN-2001 (first entry)
XX
XX Human gene single nucleotide polymorphism #387.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(11,C)
XX /*tag= a
XX /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX PN
```

```
XX 15-MAR-2001.
PD
XX
XX PF 07-SEP-2000; 2000WO-US24503.
XX
XX 10-SEP-1999; 99US-0153357.
PR 26-JUL-2000; 2000US-0220947.
PR 16-AUG-2000; 2000US-0225724.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
PI
XX WPI; 2001-226749/23.
DR
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis -
XX
XX Examples; Page 75; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification.
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 8 T; 0 other;

Query Match          1.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY . 347 TCATCGTGGTGGCCCTGTATG 367
    |||||
DB 1 TCATCGTGGTGGCCCTGTATG 21

Search completed: July 4, 2003, 07:04:56
Job time : 459 secs
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2003, 06:57:16 ; Search time 98 Seconds
(without alignments)
6305.650 Million cell updates/sec

Title: US-10-007-010-3
Perfect score: 2015
Sequence: 1 cggaggcacggaagatgagg.....atataaatgcaagtcttaag 2015

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES												
Result No.	Score	Query Match	Length	ID	Description							
C 1	18	0.9	20	2	US-08-910-629A-31	Sequence 31, Appl						
C 2	18	0.9	20	2	US-08-910-629A-42	Sequence 42, Appl						
C 3	18	0.9	20	3	US-09-209-668-7	Sequence 7, Appl						
C 4	18	0.9	20	3	US-09-287-796-31	Sequence 31, Appl						
C 5	18	0.9	20	3	US-09-287-796-42	Sequence 42, Appl						
C 6	18	0.9	20	4	US-09-130-616-31	Sequence 31, Appl						
C 7	18	0.9	20	4	US-09-130-616-42	Sequence 42, Appl						
C 8	17	0.8	20	2	US-08-730-876-2	Sequence 2, Appl						
C 9	17	0.8	20	4	US-09-490-692-71	Sequence 71, Appl						
C 10	17	0.8	23	1	US-08-222-616-2	Sequence 2, Appl						
C 11	17	0.8	23	4	US-08-446-648-2	Sequence 2, Appl						
C 12	17	0.8	23	5	PCT-US95-04228-2	Sequence 2, Appl						
C 13	16	0.8	20	4	US-09-506-073-82	Sequence 82, Appl						
C 14	16	0.8	24	2	US-08-859-998-598	Sequence 598, App						
C 15	16	0.8	24	4	US-09-225-928-598	Sequence 598, App						
C 16	15	0.7	18	3	US-08-951-923-51	Sequence 51, Appl						
C 17	15	0.7	18	4	US-08-584-040-6218	Sequence 6218, Ap						
C 18	15	0.7	19	1	US-08-400-580A-11	Sequence 11, Appl						
C 19	15	0.7	31	2	US-08-942-423-51	Sequence 51, Appl						
C 20	15	0.7	36	3	US-08-951-923-52	Sequence 52, Appl						
C 21	15	0.7	36	3	US-08-724-586-3	Sequence 3, Appl						
C 22	15	0.7	36	4	US-09-421-632-3	Sequence 3, Appl						
C 23	15	0.7	36	4	US-09-932-190-3	Sequence 3, Appl						
C 24	15	0.7	45	2	US-08-039-198B-3	Sequence 3, Appl						
C 25	15	0.7	72	2	US-08-707-237A-47	Sequence 47, Appl						
C 26	14	0.7	17	4	US-08-584-040-7661	Sequence 7661, Ap						
C 27	14	0.7	18	1	US-08-105-483-197	Sequence 197, App						

C 28	14	0.7	18	1	US-08-220-151-78	Sequence 78, Appl
C 29	14	0.7	18	1	US-08-413-118-78	Sequence 78, Appl
C 30	14	0.7	18	1	US-08-224-657-54	Sequence 54, Appl
C 31	14	0.7	18	1	US-08-709-209-197	Sequence 197, App
C 32	14	0.7	18	1	US-08-458-101-197	Sequence 197, App
C 33	14	0.7	18	2	US-08-184-009-52	Sequence 52, Appl
C 34	14	0.7	18	2	US-08-173-489C-11	Sequence 11, Appl
C 35	14	0.7	18	2	US-08-417-210A-52	Sequence 52, Appl
C 36	14	0.7	18	2	US-08-585-684B-2737	Sequence 2737, Ap
C 37	14	0.7	18	2	US-08-458-356-52	Sequence 52, Appl
C 38	14	0.7	18	3	US-08-473-446-78	Sequence 78, Appl
C 39	14	0.7	18	4	US-09-038-073-2737	Sequence 2737, Ap
C 40	14	0.7	18	4	US-08-460-736-52	Sequence 52, Appl
C 41	14	0.7	18	4	US-09-354-138-54	Sequence 54, Appl
C 42	14	0.7	20	1	US-08-639-763-6	Sequence 6, Appl
C 43	14	0.7	20	4	US-09-270-542-161	Sequence 161, App
C 44	14	0.7	20	4	US-09-798-096-87	Sequence 87, Appl
C 45	14	0.7	21	1	US-08-056-200-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-08-910-629A-31/c

; Sequence 31, Application US/08910629A

; Patent No. 5877309

; GENERAL INFORMATION:

; APPLICANT: Robert A. McKay

; APPLICANT: Nicholas M. Dean

; APPLICANT: Brett Monia

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK

; TITLE OF INVENTION: PROTEINS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Jane Massey Licata

; STREET: 66 East Main Street

; CITY: Marlton

; STATE: NJ

; COUNTRY: USA

; ZIP: 08053

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

; MEDIUM TYPE: STORAGE

; COMPUTER: PENTIUM

; OPERATING SYSTEM: WINDOWS 95

; SOFTWARE: WORDPERFECT 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/910,629A

; FILING DATE: August 13, 1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jane Massey Licata

; REGISTRATION NUMBER: 32,257

; REFERENCE/DOCKET NUMBER: ISPH-0215

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (609) 779-2400

; TELEFAX: (609) 779-8488

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; ANTI-SENSE: Yes

US-08-910-629A-31

Query Match 0.9%; Score 18; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACCTTGGCCTGGCCCGG 1317
|||||
DB 20 GACCTTGGCCTGGCCCGG 3

RESULT 2

US-08-910-629A-42
; Sequence 42, Application US/08910629A
; Patent No. 5877309

GENERAL INFORMATION:

; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK

; TITLE OF INVENTION: PROTEINS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Jane Massey Licata

; STREET: 66 East Main Street

; CITY: Marlton

; STATE: NJ

; COUNTRY: USA

; ZIP: 08053

COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

; MEDIUM TYPE: STORAGE

; COMPUTER: PENTIUM

; OPERATING SYSTEM: WINDOWS 95

; SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/910,629A

; FILING DATE: August 13, 1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jane Massey Licata

; REGISTRATION NUMBER: 32,257

; REFERENCE/DOCKET NUMBER: ISPH-0215

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (609) 779-2400

; TELEFAX: (609) 779-8488

; INFORMATION FOR SEQ ID NO: 42:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; ANTI-SENSE: NO

US-08-910-629A-42

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACCTTGGCCTGGCCCGG 1317
|||||
DB 1 GACCTTGGCCTGGCCCGG 18

RESULT 3

US-09-209-668-7/C
; Sequence 7, Application US/09209668A
; Patent No. 6114517

GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; APPLICANT: Xu, Xiaoxing S.

; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR

; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES

; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-209-668-7

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACCTTGGCCTGGCCCGG 1317
|||||
DB 20 GACCTTGGCCTGGCCCGG 3

RESULT 4

US-09-287-796-31/C
; Sequence 31, Application US/09287796A
; Patent No. 6133246

GENERAL INFORMATION:

; APPLICANT: McKay, Robert A.

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Monia, Brett

; APPLICANT: Nero, Pam

; APPLICANT: Gaarde, William A.

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

; FILE REFERENCE: ISPH-0350

; CURRENT APPLICATION NUMBER: US/09/287,796A

; CURRENT FILING DATE: 1999-04-07

; EARLIER APPLICATION NUMBER: 09/130,616

; EARLIER FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: 08/910,629

; EARLIER FILING DATE: 1997-08-03

; NUMBER OF SEQ ID NOS: 165

; SEQ ID NO 31

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sequence

US-09-287-796-31

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACCTTGGCCTGGCCCGG 1317
|||||
DB 20 GACCTTGGCCTGGCCCGG 3

RESULT 5

US-09-287-796-42
; Sequence 42, Application US/09287796A
; Patent No. 6133246

GENERAL INFORMATION:

; APPLICANT: McKay, Robert A.

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Monia, Brett

; APPLICANT: Nero, Pam

; APPLICANT: Gaarde, William A.

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

; FILE REFERENCE: ISPH-0350

; CURRENT APPLICATION NUMBER: US/09/287,796A

; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-42

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 GACTTTGGCCTGGCCCGG 1317
|||||

Db 1 GACTTTGGCCTGGCCCGG 18

RESULT 6

US-09-130-616-31/c
; Sequence 31, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

Query Match 0.9%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 GACTTTGGCCTGGCCCGG 1317
|||||

Db 20 GACTTTGGCCTGGCCCGG 3

RESULT 7

US-09-130-616-42
; Sequence 42, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

Query Match 0.9%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 GACTTTGGCCTGGCCCGG 1317
|||||

Db 1 GACTTTGGCCTGGCCCGG 18

RESULT 8

US-08-730-876-2/c
; Sequence 2, Application US/08730876
; Patent No. 5859314
; GENERAL INFORMATION:
; APPLICANT: HIBBS, Margaret L.;
; APPLICANT: DUNN, Ashley R.;
; APPLICANT: GRALL, Dianne;
; APPLICANT: HODGSON, George;
; APPLICANT: TARLINGTON, David M.;
; APPLICANT: ARMES, Jane
; TITLE OF INVENTION: ANIMALS WITH TARGETED GENE DELETION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,876
; FILING DATE: 18-Oct-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,578
; FILING DATE: 20-Oct-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5859314man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5369 - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-730-876-2

Query Match 0.8%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 916 GGCAGTTGGGGAAGT 932
|||||

Db 17 GGGCAGTTTGGGAAGT 1

RESULT 9

US-09-490-692-71/c
; Sequence 71, Application US/09490692
; Patent No. 6180353
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTS-0120
; CURRENT APPLICATION NUMBER: US/09/490,692
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-490-692-71

Query Match 0.8%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TCAGGAGGATGATGAAG 44

Db 18 TCAGGAGGATGATGAAG 2

RESULT 10

US-08-222-616-2/c
; Sequence 2, Application US/08222616
; Patent No. 5635177
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,616
; FILING DATE: 4-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00586
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/826935
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 821P2
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-616-2

Query Match 0.8%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GACGTCGTGCTCTTGG 1436

Db 23 GACGTCGTGCTCTTGG 7

RESULT 11

US-08-446-648-2/c
; Sequence 2, Application US/08446648
; Patent No. 6331302
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,648
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-446-648-2

Query Match 0.8%; Score 17; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GACGTCGTGCTCTTGG 1436
Db 23 GACGTCGTGCTCTTGG 7

RESULT 12
PCT-US95-04228-2/c
; Sequence 2, Application PC/TUS9504228
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04228
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-04228-2

Query Match 0.8%; Score 17; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GACGTCGTGCTCTTGG 1436
Db 23 GACGTCGTGCTCTTGG 7

RESULT 13
US-09-506-073-82/c
; Sequence 82, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214

; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: PCT/US98/13961
; EARLIER FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: US 08/888,982
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US 08/756,806
; EARLIER FILING DATE: 1996-11-26
; EARLIER APPLICATION NUMBER: PCT/US95/07111
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/250,856
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-506-073-82

Query Match 0.8%; Score 16; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GAGCGGCGCCAGGAT 170
Db 20 GAGCGGCGCCAGGAT 5

RESULT 14
US-08-859-998-598
; Sequence 598, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jekhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

QY 1420 GACGTCGTGCTCTTGG 1436
Db 23 GACGTCGTGCTCTTGG 7

RESULT 12
PCT-US95-04228-2/c
; Sequence 2, Application PC/TUS9504228
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04228
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-04228-2

Query Match 0.8%; Score 17; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GACGTCGTGCTCTTGG 1436
Db 23 GACGTCGTGCTCTTGG 7

RESULT 13
US-09-506-073-82/c
; Sequence 82, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214

```

; FEATURE:
; OTHER INFORMATION:.. oligonucleotide primer
US-08-859-998-598

Query Match      0.8%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 CATCCACCGAGACCTC 1251
Db      8 CATCCACCGAGACCTC 23

RESULT 15
US-09-225-928-598
; Sequence 598, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;      Johhadze, George
;      Bidilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;      EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-225-928-598

Query Match      0.8%; Score 16; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 CATCCACCGAGACCTC 1251
Db      8 CATCCACCGAGACCTC 23

Search completed: July 4, 2003, 10:39:34
Job time : 100 secs

```


Db 95 TCAAGTGGACAGCTCTCGAGCC 117
|||||

RESULT 4

US-08-237-401A-25
; Sequence 25, Application US/08237401A
; Patent No. 5837448
; GENERAL INFORMATION:
; APPLICANT: Lemke Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,401A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/884,486
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Halie Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07251/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; IMMEDIATE SOURCE:
; CLONE: Tyro-13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..147
US-08-237-401A-25

Query Match 1.1%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TCAAGTGGACAGCTCTCGAGCC 1389
|||||

Db 95 TCAAGTGGACAGCTCTCGAGCC 117

RESULT 5

US-08-306-691B-29
; Sequence 29, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.

STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-29

Query Match 1.1%; Score 23; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GATGCTGGGAGATCCCTCGGA 884
|||||

Db 87 GATGCTGGGAGATCCCTCGGA 109

RESULT 6

PCT-US93-06251-71
; Sequence 71, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-71

Query Match 1.1%; Score 23; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GATGCTGGGAGATCCCTCGGGA 884
|||||
DB 87 GATGCTGGGAGATCCCTCGGGA 109

RESULT 7
US-07-820-011A-3
Sequence 3, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1611
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 20
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio

AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
TITLE: pp60c-src
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-3

Query Match 1.1%; Score 23; DB 1; Length 1611;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 23; Conservative 0; Mismatches 0; Indels 0;

QY 862 GATGCTGGGAGATCCCTCGGGA 884
|||||
DB 781 GATGCTGGGAGATCCCTCGGGA 803

RESULT 8
PCT-US93-00445-3
Sequence 3, Application PC/TUS9300445
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399

```

; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1611
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 20
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: pp60c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUE: 5
; PAGES: 1978-1983
; DATE: May, 1987
; PCT-US93-00445-3

Query Match 1.1%; Score 23; DB 5; Length 1611;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GATCGCTGGGAGATCCCTCGGA 884
Db 781 GATCGCTGGGAGATCCCTCGGA 803

RESULT 9
US-09-173-581-12
; Sequence 12, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yuen, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina

Query Match 1.1%; Score 22; DB 3; Length 1574;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 AGGAGCCCATCTACATCATCAC 1103
Db 532 AGGAGCCCATCTACATCATCAC 553

RESULT 11
PCT-US95-08493-12
; Sequence 12, Application PC/TUS9508493
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive
; APPLICANT: Caruso, Anthony
; TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
; NUMBER-OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; APPLICANT: Gorgone, Gina
```

ADDRESSEE: LEGAL AFFAIRS
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-SEP-1996
APPLICATION NUMBER: PCT/US95/08493
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15234A
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3398 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2961
PCT-US95-08493-12

Query Match 1.0%; Score 21; DB 5; Length 3398;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 TAAGATGCTGACATGGCCT 1310
|||||
DB 2568 TAAGATGCTGACATGGCCT 2568

RESULT 12
US-08-093-383-2/c
Sequence 2, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
APPLICANT: DeBoer, Herman A.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,383
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/619827
FILING DATE: 28-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/632361
FILING DATE: 19-JUL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/303687
FILING DATE: 18-SEP-1981
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 46C4
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-093-383-2
Query Match 1.0%; Score 20; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GATGAAGACGATGACGACGA 75
|||||
DB 67 GATGAAGACGATGACGACGA 48

RESULT 13
US-08-707-793A-3
Sequence 3, Application US/08707793A
Patent No. 5776696
GENERAL INFORMATION:
APPLICANT: SALOWE, SCOTT P.
TITLE OF INVENTION: A HIGH THROUGHPUT ASSAY USING
FUSION PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,793A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Camara, Valerie J
REGISTRATION NUMBER: 35,090
REFERENCE/DOCKET NUMBER: 19494
TELEPHONE: 908-594-3502
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs

;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
US-08-707-793A-3

Query Match 1.0%; Score 20; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 GTGAACATTACAAGATCCG 707
|||||
Db 526 GTGAACATTACAAGATCCG 545

RESULT 14

US-08-707-792A-3
; Sequence 3, Application US/08707792A
; Patent No. 5783398
; GENERAL INFORMATION:
; APPLICANT: MARCY, ALICE
; APPLICANT: SALOWE, SCOTT P.
; APPLICANT: WISNIEWSKI, DOUGLAS
; TITLE OF INVENTION: A HIGH THROUGHPUT ASSAY USING
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,792A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Camara, Valerie J
REGISTRATION NUMBER: 35,090
REFERENCE/DOCKET NUMBER: 19524
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3902
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-707-792A-3

Query Match 1.0%; Score 20; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 GTGAACATTACAAGATCCG 707
|||||
Db 526 GTGAACATTACAAGATCCG 545

RESULT 15

US-09-099-053-1

; Sequence 1, Application US/09099053
; Patent No. 6388063
; GENERAL INFORMATION:
; APPLICANT: Greg Plowman
; APPLICANT: Susan Onrust
; APPLICANT: David Markby
; APPLICANT: Sara Courtneidge
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SAD RELATED DISORDERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,053
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,914
FILING DATE: June 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-099-053-1
Query Match 1.0%; Score 20; DB 4; Length 1548;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AAGTCAGACGCTCTGGTCCTT 1433
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Db 1264 AAGTCAGACGCTCTGGTCCTT 1283

Search completed: July 4, 2003, 04:49:24
Job time: 127 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: July 4, 2003, 04:49:28 ; Search time 5237 Seconds
(without alignments)
11197.662 Million cell updates/sec

Title: US-10-007-010-3
Perfect score: 2015
Sequence: 1 cggaggcagcgagatgagg.....atataaatgcaagtcttaag 2015

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Total number of hits satisfying chosen parameters: 995600

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Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	1.3	72	14	ALRSRCB	J02351 Rous sarcom
2	25	1.2	51	6	AX165171	AX165171 Sequence
3	18	0.9	19	6	AX129247	AX129247 Sequence
c 4	18	0.9	20	6	AR110470	AR110470 Sequence
c 5	18	0.9	20	6	AR116450	AR116450 Sequence
6	18	0.9	20	6	AR116461	AR116461 Sequence
c 7	18	0.9	20	6	AX104119	AX104119 Sequence
c 8	18	0.9	20	6	AX164692	AX164692 Sequence
c 9	18	0.9	20	6	AX355435	AX355435 Sequence
c 10	18	0.9	48	6	AX427069	AX427069 Sequence
c 11	18	0.9	51	6	AX427068	AX427068 Sequence
12	17	0.8	19	6	AX129246	AX129246 Sequence
c 13	17	0.8	20	6	AR029423	AR029423 Sequence
c 14	17	0.8	20	6	AR126642	AR126642 Sequence
c 15	17	0.8	21	6	AX201544	AX201544 Sequence
c 16	17	0.8	23	6	I44506	I44506 Sequence 2
c 17	17	0.8	57	6	AX179479	AX179479 Sequence
c 18	17	0.8	63	9	AF339072	AF339072 Cheirogal
c 19	17	0.8	71	4	AF055530	AF339077 Pan trogl
c 20	17	0.8	71	4	AF055530	AF055530 Didelphis
c 21	16	0.8	22	6	AX465576	AX465576 Sequence
22	16	0.8	24	6	AR090478	AR090478 Sequence
c 23	16	0.8	24	6	AR197513	AR197513 Sequence
c 24	16	0.8	64	6	A67729	A67729 Sequence 59
c 25	16	0.8	71	9	HSU38ASNR	X97582 H.sapiens s
c 26	15	0.7	18	6	AR190730	AR190730 Sequence
27	15	0.7	19	6	I77125	I77125 Sequence 11
c 28	15	0.7	31	6	AR069592	AR069592 Sequence
c 29	15	0.7	31	6	AX249143	AX249143 Sequence
c 30	15	0.7	31	6	AX249144	AX249144 Sequence
c 31	15	0.7	31	6	AX249145	AX249145 Sequence
32	15	0.7	31	6	AX249146	AX249146 Sequence
c 33	15	0.7	31	6	AX249147	AX249147 Sequence
c 34	15	0.7	36	6	AX069497	AX069497 Sequence
c 35	15	0.7	36	6	AX069498	AX069498 Sequence
c 36	15	0.7	43	6	AX141093	AX141093 Sequence
37	15	0.7	43	6	AX146963	AX146963 Sequence
c 38	15	0.7	44	6	AX473094	AX473094 Sequence
c 39	15	0.7	45	6	AR028569	AR028569 Sequence
40	15	0.7	48	6	A18448	A18448 oligonucleo
c 41	15	0.7	51	6	AX159179	AX159179 Sequence
c 42	15	0.7	51	6	AX159180	AX159180 Sequence
c 43	15	0.7	51	6	AX199202	AX199202 Sequence
c 44	15	0.7	60	6	AX455886	AX455886 Sequence
c 45	15	0.7	65	6	AX482877	AX482877 Sequence

ALIGNMENTS

RESULT 1	ALRSRCB	ALRSRCB	72 bp ss-RNA	linear	VRL 28-APR-1993
LOCUS	Rous sarcoma virus (RSV) src gene, partial.				
DEFINITION	J02351				
ACCESSION	J02351.1	GI:210266			
VERSION	c-myc proto-oncogene; kinase; protein kinase; src oncogene.				
KEYWORDS	Rous sarcoma virus (Prague A strain) DNA, clones pCH1.pCH7 & pCH20.				
SOURCE	Rous sarcoma virus				
ORGANISM	Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.				
REFERENCE	1 (bases 1 to 72)				
AUTHORS	Bryant, D. and Parsons, J.T.				
TITLE	Site-directed point mutation in the src gene of rous sarcoma virus results in an inactive src gene product				
JOURNAL	J. Virol. 45 (3), 1211-1216 (1983)				

MEDLINE 83164366
PUBMED 6300458
COMMENT A 'g' to 'a' transition at base 55 results in the incorporation of Thr instead of Ala at amino acid 433. This change decreases the protein kinase activity of the product and abolishes the pp60-src mediated cellular transformation activity.

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/organism="Rous sarcoma virus"
/db_xref="taxon:11886"
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/note="v-src protein"
/codon_start=1
/protein_id="AAA42584.1"
/db_xref="GI:210267"
/translation="EYTAHQAKFKIKWTAPEALYGR"
BASE COUNT 17 a 25 c 21 g 9 t
ORIGIN 52 bp upstream of BglII site.

Query Match 1.3%; Score 26; DB 14; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCCAAGTCCCCATCAAGTGGACGC 1379
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Db 22 GCCAAGTCCCCATCAAGTGGACGC 47

RESULT 2
AX15171
LOCUS AX15171 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 366 from Patent WO0138586.
ACCESSION AX15171
VERSION AX15171.1 GI:14546000
KEYWORDS human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 366 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 26
/note="single nucleotide polymorphism
Accession number cg42665067"
BASE COUNT 10 a 17 c 13 g 11 t
ORIGIN

Query Match 1.2%; Score 25; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 GGGGCTTCTACATATCCCCCGAAG 746
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Db 1 GGGGCTTCTACATATCCCCCGAAG 25

RESULT 3
AX129247
LOCUS AX129247 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 465 from Patent WO0130362.
ACCESSION AX129247
VERSION AX129247.1 GI:14135552
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 465 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source 1..19
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cdk4 ribozyme binding site"
BASE COUNT 1 a 6 c 7 g 5 t
ORIGIN

Query Match 0.9%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 GCTGACTTTGGCTGGCC 1314
|||||
Db 2 GCTGACTTTGGCTGGCC 19

RESULT 4
AR110470/c
LOCUS AR110470 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6114517.
ACCESSION AR110470
VERSION AR110470.1 GI:12826746
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P. and Xu, X.S.
TITLE Methods of modulating tumor necrosis factor alpha.-induced expression of cell adhesion molecules
JOURNAL Patent: US 6114517-A 7 05-SEP-2000;
FEATURES
source 1..20
/organism="unknown"
BASE COUNT 4 a 7 c 7 g 2 t
ORIGIN

Query Match 0.9%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCTGGCCCGG 1317
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Db 20 GACTTTGGCTGGCCCGG 3

RESULT 5
AR116450/c
LOCUS AR116450 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6133246.
ACCESSION AR116450
VERSION AR116450.1 GI:14096772
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Dean, N., Monia, B.P., Nero, P.S. and Gaarde, W.A.
TITLE Antisense oligonucleotide compositions and methods for the modulation of JNK proteins
JOURNAL Patent: US 6133246-A 31 17-OCT-2000;
FEATURES
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BASE COUNT      4 a      7 c      7 g      2 t
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Query Match      0.9%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1300 GACTTTGGCCTGGCCCGG 1317
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Db      20 GACTTTGGCCTGGCCCGG 3

RESULT 6
LOCUS      AR116461
DEFINITION Sequence 42 from patent US 6133246.
ACCESSION  AR116461
VERSION     AR116461.1 GI:14096783
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE      Antisense oligonucleotide compositions and methods for the
JOURNAL    modulation of JNK proteins
PATENT     US 6133246-A 42 17-OCT-2000;
FEATURES    Location/Qualifiers
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            /organism="unknown"
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BASE COUNT      2 a      7 c      7 g      4 t
ORIGIN
Query Match      0.9%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1300 GACTTTGGCCTGGCCCGG 1317
      |||||||
Db      1 GACTTTGGCCTGGCCCGG 18

RESULT 7
LOCUS      AX104119/c
DEFINITION Sequence 311 from Patent WO0122972.
ACCESSION  AX104119
VERSION     AX104119.1 GI:13920316
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE      Immunostimulatory nucleic acids
JOURNAL    Patent: WO 0122972-A 311 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES    Location/Qualifiers
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BASE COUNT      4 a      7 c      7 g      2 t
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1300 GACTTTGGCCTGGCCCGG 1317
      |||||||
Db      20 GACTTTGGCCTGGCCCGG 3

RESULT 8
LOCUS      AX164692/c
DEFINITION Sequence 2 from Patent WO0134792.
ACCESSION  AX164692
VERSION     AX164692.1 GI:14545586
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Potapova,O., Gorospe,M. and Holbrook,N.J.
TITLE      Compositions and methods for the diminution or elimination of
JOURNAL    various cancers
PATENT     WO 0134792-A 2 17-MAY-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES    Location/Qualifiers
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            /note="Synthetic"
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BASE COUNT      4 a      7 c      7 g      2 t
ORIGIN
Query Match      0.9%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      20 GACTTTGGCCTGGCCCGG 3

RESULT 9
LOCUS      AX355435/c
DEFINITION Sequence 463 from Patent WO0197843.
ACCESSION  AX355435
VERSION     AX355435.1 GI:18620103
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS    Weiner,G. and Hartmann,G.
TITLE      Methods for enhancing antibody-induced cell lysis and treating
JOURNAL    cancer
PATENT     WO 0197843-A 463 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES    Location/Qualifiers
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            /note="Synthetic oligonucleotide-phosphorothioate
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            4 a      7 c      7 g      2 t

BASE COUNT      4 a      7 c      7 g      2 t
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1300 GACTTTGGCCTGGCCCGG 1317
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Db      20 GACTTTGGCCTGGCCCGG 3

RESULT 10
LOCUS      AX427069/c
DEFINITION Sequence 33 from Patent WO0196604.
ACCESSION  AX427069
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VERSION AX427069.1 GI:21530452
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
TITLE Assay for genetic polymorphisms using scattered light detectable labels
JOURNAL Patent: WO 0196604-A 33 20-DEC-2001;
GENICON Sciences Corporation (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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BASE COUNT 9 a 20 c 10 g 9 t
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Matches 18; Conservative 0;
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LOCUS AX427068 51 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 32 from Patent WO0196604.
ACCESSION AX427068
VERSION AX427068.1 GI:21530451
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
TITLE Assay for genetic polymorphisms using scattered light detectable labels
JOURNAL Patent: WO 0196604-A 32 20-DEC-2001;
GENICON Sciences Corporation (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
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/note="Exemplary probe for CYP2D6 allele detection"
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Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
QY 1003 GAGGCCTTCTGGCAGAG 1020
Db 48 GAGGCCTTCTGGCAGAG 31
RESULT 12
AX129246
LOCUS AX129246 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 464 from Patent WO0130362.
ACCESSION AX129246
VERSION AX129246.1 GI:14135551
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 464 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/note="cdk4 ribozyme binding site"
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Best Local Similarity 100.0%; Pred. No. 1.8e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;
QY 1297 GCTGACTTTGGCCTGGC 1313
Db 3 GCTGACTTTGGCCTGGC 19
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LOCUS AR029423 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5859314.
ACCESSION AR029423
VERSION AR029423.1 GI:5941396
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hibbs,M.L., Dunn,A.R., Graill,D., Hodgson,G., Tarlington,D.M. and Ames,J.
TITLE Mice with targeted tyrosine kinase, lyn, disruption
JOURNAL Patent: US 5859314-A 2 12-JAN-1999;
FEATURES Location/Qualifiers
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/organism="unknown"
BASE COUNT 4 a 10 c 2 g 4 t
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Best Local Similarity 100.0%; Pred. No. 1.8e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;
QY 916 GGCAGTTTGGGGAAGT 932
Db 17 GGCAGTTTGGGGAAGT 1
RESULT 14
AR126642/c
LOCUS AR126642 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 71 from patent US 6180353.
ACCESSION AR126642
VERSION AR126642.1 GI:14113235
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Cowser,L.M.
TITLE Antisense modulation of dxxx expression
JOURNAL Patent: US 6180353-A 71 30-JAN-2001;
FEATURES Location/Qualifiers
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BASE COUNT 3 a 9 c 1 g 7 t
ORIGIN
Query Match 0.8%; Score 17; DB 6; Length 20;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: July 4, 2003, 06:11:39 ; Search time 2904 Seconds

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Title: US-10-007-010-3

Perfect score: 2015

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Maximum DB seq length: 100

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- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_estl.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: gb_gss.*
- 18: em_gss_hum.*
- 19: em_gss_inv.*
- 20: em_gss_pla.*
- 21: em_gss_vrt.*
- 22: em_gss_fun.*
- 23: em_gss_mam.*
- 24: em_gss_mus.*
- 25: em_gss_Other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18	0.9	93	10	AW238943	AW238943 xb29h03.y
2	17	0.8	52	12	BF636617	BF636617 NF091E04D
3	16	0.8	53	13	BJ048171	BJ048171 BJ048171
4	16	0.8	56	17	AZ801785	AZ801785 2M0060E22
5	16	0.8	64	9	AA117806	AA117806 mo65a02.r
6	16	0.8	66	9	AI906791	AI906791 IL-BT125-

c	7	16	0.8	66	9	AI906801	AI906801 RC-BT125-
c	8	16	0.8	66	9	AI906818	AI906818 RC-BT125-
c	9	16	0.8	67	9	AA235459	AA235459 zt31a12.s
c	10	16	0.8	68	10	AV832681	AV832681 AV832681
c	11	16	0.8	72	17	B35762	B35762 HS-1030-B1-
c	12	16	0.8	73	17	BH801576	BH801576 1008117H1
c	13	16	0.8	79	13	BJ034007	BJ034007 BJ034007
c	14	16	0.8	82	9	AA761095	AA761095 ny13h05.s
c	15	16	0.8	88	9	AA620617	AA620617 af84b06.s
c	16	16	0.8	97	14	H61808	H61808 yu41c09.s1
c	17	15	0.7	33	10	AW059793	AW059793 LESg11.yg
c	18	15	0.7	36	14	D12082	D12082 HUM0S16A04
c	19	15	0.7	44	14	D19127	D19127 HUM0S01342
c	20	15	0.7	44	17	BH643552	BH643552 1008058F0
c	21	15	0.7	54	17	B33982	B33982 HS-1023-B2-
c	22	15	0.7	55	14	R54182	R54182 yg98b12.r1
c	23	15	0.7	55	17	BH415966	BH415966 1007045F1
c	24	15	0.7	58	13	BM307600	BM307600 sak31d09.f
c	25	15	0.7	58	14	C01969	C01969 HUMG5000398
c	26	15	0.7	59	13	BM018730	BM018730 603646626
c	27	15	0.7	61	14	C02010	C02010 HUMG5000453
c	28	15	0.7	62	14	H25116	H25116 y143b09.s1
c	29	15	0.7	62	17	TA158A09P	TA158A09P T. brucei
c	30	15	0.7	63	17	AZ307924	AZ307924 IM0010E24
c	31	15	0.7	64	10	BE636462	BE636462 SMOVL2CAS
c	32	15	0.7	64	17	AZ960593	AZ960593 2M0228N10
c	33	15	0.7	67	9	AL644576	AL644576 AL644576
c	34	15	0.7	70	9	AI215407	AI215407 qb07f12.x
c	35	15	0.7	74	17	CNS030KY	AI222379 Tetraodon
c	36	15	0.7	75	14	F33772	F33772 HSPD27429.H
c	37	15	0.7	75	17	AZ467917	AZ467917 IM0279E08
c	38	15	0.7	76	9	AA826784	AA826784 nr89f05.s
c	39	15	0.7	77	9	AA743582	AA743582 ny29c01.s
c	40	15	0.7	80	9	AA930335	AA930335 VS59c04.r
c	41	15	0.7	81	9	AA585407	AA585407 PTH327A.H
c	42	15	0.7	81	17	AF179956	AF179956 AF179956
c	43	15	0.7	84	17	B40784	B40784 HS-1052-B1-
c	44	15	0.7	84	17	CNS03YXT	AL266906 Tetraodon
c	45	15	0.7	85	10	AV533467	AV533467 AV533467

ALIGNMENTS

RESULT 1
AW238943
LOCUS
DEFINITION
93 bp mRNA linear EST 13-DEC-1999
xb29h03.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2577749 5'
similar to gb:X12597 HIGH MOBILITY GROUP PROTEIN HMGL (HUMAN
); contains element THR repetitive element ; , mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW238943
1 (bases 1 to 93)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other_ESTs: xb29h03.x1
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40RP from Gibco

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FEATURES
  source
    High quality sequence stop: 86.
    Location/Qualifiers
      1. .93
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:2577749"
      /clone_lib="NCI_CGAP_Lu31"
      /sex="male"
      /dev_stage="fetal, 14 wk post-conception"
      /lab_host="DHI0B"
      /note="Organ: lung, cell line; Vector: pCMV-SPORT6;
      Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally, no
      5' adaptor. Primer: Oligo dr. Full-length library
      constructed by Life Technologies."
      46 a      8 c      30 g      9 t
      ORIGIN
        Query Match      0.9%; Score 18; DB 10; Length 93;
        Best Local Similarity 100.0%; Pred. No. 8.6e+02;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGATGAGGAGATGA 27          52 bp mRNA linear EST 19-DEC-2000
      |||||
Db 75 GGAAGATGAGGAGATGA 92          5', mRNA sequence.

RESULT 2
BF636617/c
LOCUS
DEFINITION
  BF636617
  52 bp mRNA linear EST 19-DEC-2000
ACCESSION
  BF636617
VERSION
  BF636617.1 GI:11900775
KEYWORDS
  EST.
SOURCE
  Medicago truncatula
  barrel medic.
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
  1 (bases 1 to 52)
REFERENCE
  Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
  Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula drought library
  Unpublished (2000)
JOURNAL
  Contact: May GD
COMMENT
  Plant Biology Division
  The Samuel Roberts Noble Foundation
  2510 Sam Noble Parkway, Ardmore, OK 73402, USA
  Tel: 580 221 7391
  Fax: 580 221 7380
  Email: gdmay@noble.org
  Insert Length: 52 Std Error: 0.00
  Plate: 091 row: E column: 04
  Seq primer: TCACACAGGAGACGATGAC.

FEATURES
  source
    Location/Qualifiers
      1. .52
      /organism="Medicago truncatula"
      /db_xref="taxon:3880"
      /clone="NF091E04Dt"
      /clone_lib="Drought"
      /tissue_type="Plantlets"
      /dev_stage="Pooled timepoints"
      /note="Vector: Lambda Zap; Contains a mixture of entire
      plantlets harvested in a series of days-post-watering
      timepoints."
      12 a      5 c      2 g      22 t      11 others
      ORIGIN

Query Match      0.8%; Score 17; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1966 AAAATAGTGAATGAAT 1982
      |||||
Db 39 AAAATAGTGAATGAAT 23

RESULT 3
BJ048171
LOCUS
DEFINITION
  BJ048171
  53 bp mRNA linear EST 07-DEC-2001
  laevis cDNA clone XL018016 3', mRNA sequence.
ACCESSION
  BJ048171
VERSION
  BJ048171.1 GI:17406228
KEYWORDS
  EST.
SOURCE
  African clawed frog.
  Xenopus laevis
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
  Xenopodinae; Xenopus.
  1 (bases 1 to 53)
REFERENCE
  Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
  Y.
  Expressed genes in X. laevis embryo
  Unpublished (2001)
JOURNAL
  Contact: Tadasu Shin-i
COMMENT
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.

FEATURES
  source
    Location/Qualifiers
      1. .53
      /organism="Xenopus laevis"
      /db_xref="taxon:8355"
      /clone="XL018016"
      /clone_lib="NIBB Mochii normalized Xenopus neurula
      library"
      /tissue_type="whole embryo"
      /dev_stage="stage 15"
      /note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
      were oligo-dT primed and directionally cloned. Staging
      according to Nieukoop and Faber. Library is subtracted
      and was constructed by N. Garrett and A.M. Zorn,
      (Wellcome/CRC Institute)."
      16 a      9 c      13 g      11 t      4 others
      ORIGIN

Query Match      0.8%; Score 16; DB 13; Length 53;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 AGAAGCCTGGGAGAA 860
      |||||
Db 20 AGAAGCCTGGGAGAA 35

RESULT 4
AZ801785
LOCUS
DEFINITION
  AZ801785
  56 bp DNA linear GSS 16-FEB-2001
  Clone UUGC2M0060E22 F, DNA sequence.
ACCESSION
  AZ801785
VERSION
  AZ801785.1 GI:12954108
KEYWORDS
  GSS.
SOURCE
  house mouse.
  Mus musculus
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 56)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

```

TITLE
JOURNAL
COMMENT

and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: E column: 22
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 56.
Location/Qualifiers
1. .56
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0060E22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 18 a 3 c 24 g 11 t
ORIGIN

Query Match 0.8%; Score 16; DB 17; Length 56;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GTGAGAGGGAGATCA 60
|||||
Db 12 GTGAGAGGGAGATCA 27

RESULT 5
LOCUS AA117806 64 bp mRNA linear EST 15-FEB-1997
DEFINITION mo58a02.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:558410 5', mRNA sequence.
ACCESSION AA117806
VERSION AA117806.1 GI:1672822
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 64)
REFERENCE Maria.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

TITLE
JOURNAL
COMMENT

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:339202
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 52.
Location/Qualifiers
1. .64
/organism="Mus musculus"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:558410"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site:1:
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5',
adaptor sequence: 5' GAATTCGGCAGGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

BASE COUNT 26 a 3 c 29 g 6 t
ORIGIN

Query Match 0.8%; Score 16; DB 9; Length 64;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GAAGGTGAAGAGGGAG 56
|||||
Db 27 GAAGGTGAAGAGGGAG 42

RESULT 6
LOCUS AI906791 66 bp mRNA linear EST 30-MAR-2000
DEFINITION IL-BT125-090299-004 BT125 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI906791
VERSION AI906791.1 GI:6497199
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 66)
REFERENCE Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=ILat2=IL-BT125-004.html
&t3=090299&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1. .66
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT125"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
15 a 12 c 21 g 15 t

BASE COUNT 18 a 12 c 21 g 15 t
ORIGIN

Query Match 0.8%; Score 16; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 GATGCGCTGCTGGAAA 1590
|||||
Db 45 GATGCGCTGCTGGAAA 60

RESULT 7
AI906801/c
LOCUS
DEFINITION RC-BT125-030399-008 BT125 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI906801
VERSION AI906801.1 GI:6497209
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 66)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zaglo,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT125-008.html
&t3=030399&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1. .66
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT125"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
18 a 12 c 21 g 15 t

BASE COUNT 18 a 12 c 21 g 15 t
ORIGIN

Query Match 0.8%; Score 16; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 GATGCGCTGCTGGAAA 1590
|||||
Db 45 GATGCGCTGCTGGAAA 60

RESULT 8
AI906818
LOCUS
DEFINITION RC-BT125-040399-020 BT125 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI906818
VERSION AI906818.1 GI:6497226
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 66)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zaglo,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT125-020.html
&t3=040399&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1. .66
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT125"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
18 a 12 c 21 g 15 t

BASE COUNT 18 a 12 c 21 g 15 t
ORIGIN

University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT810 row: D column: 3
Class: BAC ends
High quality sequence stop: 72.

FEATURES

source

Location/Qualifiers

1. .72
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate-CT810 Col-3 Row-D"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 13 a 20 c 17 g 21 t 1 others
ORIGIN

Query Match 0.8%; Score 16; DB 17; Length 72;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1020 GGCCAAAGTGATGAAA 1035
|||||
Db 60 GGCCAAAGTGATGAAA 45

RESULT 12

BH801576

LOCUS

DEFINITION BH801576 73 bp DNA linear GSS 25-APR-2002
1008117H12.2EL_y1 1008 - RescueMu Grid I Zea mays genomic, DNA sequence.

ACCESSION BH801576

VERSION BH801576.1 GI:20314787

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 73)

REFERENCE

AUTHORS Walbot, V.

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008117 row: 20
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers

1. .73
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web

site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 22 a 19 c 22 g 10 t
ORIGIN

Query Match 0.8%; Score 16; DB 17; Length 73;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 AAGACGATGACGACGA 75
|||||

Db 1 AAGACGATGACGACGA 16
|||||

RESULT 13

BJ034007

LOCUS

DEFINITION BJ034007 NIBB Mochii normalized Xenopus neurula library EST 05-DEC-2001
laevis cDNA clone XL025010 5', mRNA sequence.

ACCESSION BJ034007

VERSION BJ034007.1 GI:17379716

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 79)

REFERENCE 1 (bases 1 to 79)

AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.

TITLE Expressed genes in x. laevis embryo

JOURNAL Unpublished (2001)

COMMENT Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. .79

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="XL025010"

/clone_lib="NIBB Mochii normalized Xenopus neurula library"

/tissue_type="whole embryo"

/dev_stage="stage 15"

/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; CDNAS were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

(Wellcome/CRC Institute)."

BASE COUNT 17 a 14 c 25 g 23 t
ORIGIN

Query Match 0.8%; Score 16; DB 13; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 TCTGAGGGGACCTCAG 95
|||||

Db 55 TCTGAGGGGACCTCAG 70
|||||

RESULT 14

AA761095/c

LOCUS

DEFINITION nyl3105.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1271673 3'

82 bp mRNA linear EST 07-FEB-1998

similar to SW:GLI4_HUMAN P10075 GLI4 PROTEIN ;, mRNA sequence.

AA761095
VERSION AA761095.1 GI:2810025
KEYWORDS EST.
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 82)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio-llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1924 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source Location/Qualifiers
1..82
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1271673"
/clone_lib="NCI-CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAAGTGGAGCGCGCCATTTTTTTTTTTT-3', J. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 7 a 35 c 22 g 18 t

ORIGIN
Query Match 0.8%; Score 16; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GGGCTGCCGAGCTGGG 111
|||||
Db 69 GGGCTGCCGAGCTGGG 54

RESULT 15
AA620617/c
LOCUS
DEFINITION af84b06.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1048691
3' similar to SW:RR4_HUMAN P10075 HKR4 PROTEIN ;, mRNA sequence.
ACCESSION AA620617
VERSION AA620617.1 GI:2524556
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 88)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, J., Waterston, R. and Wilson, R.
TITLE WashU-NCI human EST project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyt not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source Location/Qualifiers
1..88
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1048691"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAAGTGGAGCGCGCCATTTTTTTTTTTT-3', J. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library went through one round of normalization to Cots5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 17 a 33 c 25 g 13 t

ORIGIN
Query Match 0.8%; Score 16; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GGGCTGCCGAGCTGGG 111
|||||
Db 75 GGGCTGCCGAGCTGGG 60

Search completed: July 4, 2003, 10:37:47
Job time : 2908 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2003, 06:57:16 ; Search time 98 Seconds
(without alignments)
6305.650 Million cell updates/sec

Title: US-10-007-010-3

Perfect score: 2015

Sequence: 1 cggaggcgcgaagatgagg.....atatataatgcaagtcttacg 2015

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2.6/prodata/1/ina/5A_COMB.seq.*
- 2: /cgn2.6/prodata/1/ina/5B_COMB.seq.*
- 3: /cgn2.6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2.6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2.6/prodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2.6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	18	0.9	20	2 US-08-910-629A-31	Sequence 31, Appl
c 2	18	0.9	20	2 US-08-910-629A-42	Sequence 42, Appl
c 3	18	0.9	20	3 US-09-209-668-7	Sequence 7, Appl
c 4	18	0.9	20	3 US-09-287-796-31	Sequence 31, Appl
c 5	18	0.9	20	3 US-09-287-796-42	Sequence 42, Appl
c 6	18	0.9	20	4 US-09-130-616-31	Sequence 31, Appl
c 7	18	0.9	20	4 US-09-130-616-42	Sequence 42, Appl
c 8	17	0.8	20	4 US-08-730-876-2	Sequence 2, Appl
c 9	17	0.8	20	4 US-09-490-692-71	Sequence 71, Appl
c 10	17	0.8	23	1 US-08-222-616-2	Sequence 2, Appl
c 11	17	0.8	23	4 US-08-446-648-2	Sequence 2, Appl
c 12	17	0.8	23	5 PCT-US95-04228-2	Sequence 2, Appl
c 13	16	0.8	20	4 US-09-506-073-82	Sequence 82, Appl
c 14	16	0.8	24	2 US-08-859-998-598	Sequence 598, App
c 15	16	0.8	24	4 US-09-225-928-598	Sequence 598, App
c 16	15	0.7	18	3 US-08-951-923-51	Sequence 51, Appl
c 17	15	0.7	18	4 US-08-584-040-6218	Sequence 6218, Ap
c 18	15	0.7	19	1 US-08-400-580A-11	Sequence 11, Appl
c 19	15	0.7	31	2 US-08-942-423-51	Sequence 51, Appl
c 20	15	0.7	36	3 US-08-951-923-52	Sequence 52, Appl
c 21	15	0.7	36	3 US-08-724-586-3	Sequence 3, Appl
c 22	15	0.7	36	4 US-09-421-632-3	Sequence 3, Appl
c 23	15	0.7	36	4 US-09-932-190-3	Sequence 3, Appl
c 24	15	0.7	45	2 US-08-039-198B-3	Sequence 3, Appl
c 25	15	0.7	72	2 US-08-707-237A-47	Sequence 47, Appl
c 26	14	0.7	17	4 US-08-584-040-7661	Sequence 7661, Ap
c 27	14	0.7	18	1 US-08-105-483-197	Sequence 197, App

Sequence 78, Appl
Sequence 78, Appl
Sequence 54, Appl
Sequence 197, App
Sequence 52, Appl
Sequence 11, Appl
Sequence 52, Appl
Sequence 2737, Ap
Sequence 52, Appl
Sequence 78, Appl
Sequence 2737, Ap
Sequence 52, Appl
Sequence 54, Appl
Sequence 6, Appl
Sequence 161, App
Sequence 87, Appl
Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-910-629A-31/c
; Sequence 31, Application US/08910629A
; Patent No. 5877309
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-910-629A-31

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 20 GACTTTGGCCTGGCCCGG 3

RESULT 2

US-08-910-629A-42
; Sequence 42, Application US/08910629A
; Patent No. 5877309
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
; TITLE OF INVENTION: PROTEINS

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESS: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: PENTIUM
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,629A
FILING DATE: August 13, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0215
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No

US-08-910-629A-42
Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 1 GACTTTGGCCTGGCCCGG 18

RESULT 3

US-09-209-668-7/c
; Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES

; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-209-668-7

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 20 GACTTTGGCCTGGCCCGG 3

RESULT 4

US-09-287-796-31/c
; Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-31

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 20 GACTTTGGCCTGGCCCGG 3

RESULT 5

US-09-287-796-42
; Sequence 42, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A

; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-42

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 1 GACTTTGGCCTGGCCCGG 18

RESULT 6

US-09-130-616-31/c
; Sequence 31, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

Query Match 0.9%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 20 GACTTTGGCCTGGCCCGG 3

RESULT 7

US-09-130-616-42
; Sequence 42, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

Query Match 0.9%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 GACTTTGGCCTGGCCCGG 1317
|||||
Db 1 GACTTTGGCCTGGCCCGG 18

RESULT 8

US-08-730-876-2/c
; Sequence 2, Application US/08730876
; Patent No. 5859314
; GENERAL INFORMATION:
; APPLICANT: HIBBS, Margaret L.;
; APPLICANT: DUNN, Ashley R.;
; APPLICANT: GRAILL, Dianne;
; APPLICANT: HODGSON George;
; APPLICANT: TADLINGTON, David M.;
; APPLICANT: ARMES, Jane
; TITLE OF INVENTION: ANIMALS WITH TARGETED GENE DELETION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,876
; FILING DATE: 18-Oct-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,578
; FILING DATE: 20-Oct-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5859314man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5369 - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-730-876-2

Query Match 0.8%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 GGGCAGTTTGGGGAAGT 932
|||||

Db 17 GGCACGTTGGGAAGT 1

RESULT 9

US-09-490-692-71/c

; Sequence 71, Application US/09490692

; Patent No. 6180353

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION

; FILE REFERENCE: RTS-0120

; CURRENT APPLICATION NUMBER: US/09/490,692

; CURRENT FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 176

; SEQ ID NO 71

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-490-692-71

Query Match 0.8%; Score 17; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TCAGGAGGATGATGAAG 44

|||||

Db 18 TCAGGAGGATGATGAAG 2

RESULT 10

US-08-222-616-2/c

; Sequence 2, Application US/08222616

; Patent No. 5635177

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,616

; FILING DATE: 4-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00586

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/826935

; FILING DATE: 22-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 821P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-222-616-2

Query Match 0.8%; Score 17; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GAGCTCTGTCCTTTGG 1436

|||||

Db 23 GAGCTCTGTCCTTTGG 7

RESULT 11

US-08-446-648-2/c

; Sequence 2, Application US/08446648

; Patent No. 6331302

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,648

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/222616

; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

US-08-446-648-2

Query Match 0.8%; Score 17; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GACGCTGGTCTTGG 1436
Db 23 GACGCTGGTCTTGG 7

RESULT 12
PCT-US95-04228-2/c
; Sequence 2, Application PC/TUS9504228
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04228
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00.000
; REFERENCE/DOCKET NUMBER: 821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/223-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-04228-2

Query Match 0.8%; Score 17; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 GACGCTGGTCTTGG 1436
Db 23 GACGCTGGTCTTGG 7

RESULT 13
US-09-506-073-82/c
; Sequence 82, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214

; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: PCT/US98/13961
; EARLIER FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: US 08/888,982
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US 08/756,806
; EARLIER FILING DATE: 1996-11-26
; EARLIER APPLICATION NUMBER: PCT/US95/07111
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/250,856
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-506-073-82

Query Match 0.8%; Score 16; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GAGCGGGCGCCAGGAT 170
Db 20 GAGCGGGCGCCAGGAT 5

RESULT 14
US-08-859-998-598
; Sequence 598, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Johhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

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;
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-598

Query Match          0.8%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1236 CATCCACCGAGACCTC 1251
Db      8 CATCCACCGAGACCTC 23

RESULT 15
US-09-225-928-598
; Sequence 598, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;              Jokhadze, George
;              Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;              EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/225,928
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-225-928-598

Query Match          0.8%; Score 16; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1236 CATCCACCGAGACCTC 1251
Db      8 CATCCACCGAGACCTC 23
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Search completed: July 4, 2003, 10:39:34
Job time : 100 secs

Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TCAGGAGGATGATGAAG 44
|||||
Db 18 TCAGGAGGATGATGAAG 2

RESULT 15
AX201544/c
LOCUS AX201544 21 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 223 from Patent WO0153486.
ACCESSION AX201544
VERSION AX201544.1 GI:15391386
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 223 26-JUL-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
1..21
source
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe."
BASE COUNT 7 a 8 c 3 g 3 t
ORIGIN

Query Match. 0.8%; Score 17; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 907 CTTGGAGCTGGGCACTT 923
|||||
Db 19 CTTGGAGCTGGGCACTT 3

Search completed: July 4, 2003, 08:32:26
Job time : 5240 secs

